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(54) Title: IMPROVED PHYTASES (57) Abstract <p>This invention relates to improved phytases, preferably phytases of an increased thermostability, and a process of producing them. In particular, stabilizing amino acid mutations are introduced into a homologous protein, or the active site of a phytase is replaced in part or in total. The corresponding DNA sequences and methods of preparing them are also disclosed, as are methods of producing the improved phytases, and the use thereof. Specific variants of <i>Aspergillus fumigatus</i> phytase and of consensus phytases are disclosed.</p>		

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Improved phytases

Phytases are enzymes that hydrolyze phytate (myo-inositol hexakisphosphate) to myo-inositol and inorganic phosphate. They
5 are known to be valuable feed additives.

The present invention relates to improved phytases, viz. phytases of amended characteristics, e.g. amended activity characteristics, reference being made to e.g. the phytase(s) it has been derived from, or to known phytases. Amended activity
10 characteristics means amended in at least one phytase activity related respect, such as (non-exclusive list): pH stability, temperature stability, pH profile, temperature profile, specific activity (in particular in relation to pH and temperature), substrate specificity, substrate cleavage pattern, substrate
15 binding, position specificity, the velocity and level of release of phosphate from corn, reaction rate, phytate degradation rate), end level of released phosphate reached.

Examples of amended activity characteristics are amended specific activity (e.g. increased, e.g. increased at a pH of 3,
20 4, 5, or 6); amended pH or temperature profile; and/or amended (e.g. increased) thermostability, e.g. of an increased melting temperature as measured using Differential Scanning Calorimetry (DSC).

The present invention also relates to a process for the
25 preparation of a modified protein, wherein in a first step a consensus sequence is determined from a number of highly homologous sequences according to steps a), b) and c) below:

a) at least three, preferably at least four amino acid sequences are aligned by any standard alignment program known in
30 the art;

b) at every position of the amino acid sequence alignment, the amino acids are evaluated for their evolutionary similarity and a consensus residue is chosen by any standard program known in the art, whereby the minimal requirements for calculation of
5 a consensus residue are set in such a way that the program is already able to determine a consensus residue if a given residue occurs in only two of the aligned sequences. However, if there is a subgroup of sequences among the compared amino acid sequences that shows a much higher degree of similarity with
10 each other than with the remaining sequences of the alignment, the subgroup may be represented in the calculation only with its consensus sequence determined in the same way as outlined in EP 897985, or alternatively, to each sequence of the subgroup, a vote weight of 1 divided by the number of sequences in the
15 subgroup will be assigned;

c) in case no consensus amino acid at a defined position is identified by the program, any of the amino acids, preferably the most frequently occurring amino acid at this position is selected.

20 In a second aspect of the invention, a homologous sequence is compared with the consensus sequence, and one or more non-consensus residues in this homologous sequence are replaced by the corresponding consensus residues.

Preferably, only such amino acid residues are replaced in
25 the homologous amino acid sequence where a consensus residue can clearly be defined by the program under moderately stringent conditions whereas at all positions of the alignment where no preferred consensus amino acid can be determined under moderately stringent conditions, the amino acids of the
30 homologous protein remain unchanged.

In a third aspect of the invention, the active center of the protein of interest is determined, comprising all amino acid residues that are involved in forming the active center, both in the consensus sequence, and in the sequence of a homologous protein; subsequently, some or all of the divergent amino acid residues of the homologous protein are inserted in the backbone of the consensus sequence.

In one embodiment of this process, the program used for the comparison of amino acids at a defined position regarding their evolutionary similarity is the program "PRETTY".

The active center of the protein can be determined by using an analysis of the three-dimensional structure of the protein.

An example of a homologous protein is an enzyme family, an example of a defined protein family is the family of phytases, e.g. of fungal origin.

For example, the amino acid sequence of the phytase can be changed by the introduction of at least one mutation or substitution chosen from

20	E58A	F54Y
	D69K	I73V
	D197N	K94A
	T214L	R101A
	E222T	N153K
25	E267D	V158I
	R291I	A203G
	R329H	S205G
	S364T	V217A
	A379K	A227V
30	G404A	V234L
		P238A

Q277E
A287H
A292Q
V366I
5 A396S
E415Q
G437A
R451E

For interpreting these abbreviations, as an example, the
10 mutation E58A is to be interpreted as follows: When subtracting
26 from the number, you get the position or residue number in
the consensus phytase sequence or another phytase sequence
aligned as shown in Fig. 1 (corresponding to the addition of a
26 amino acid signal sequence to the sequences shown in Fig. 1).
15 For example, in E58A, number 58 means position number 32 ($58 - 26 = 32$). And the letter before the number, i.e. E, represents the
amino acid in the phytase to be modified which is replaced by
the amino acid behind the number, i.e. A.

The above-mentioned amino acid replacements, alone and/or
20 in combination, have a positive effect on the protein stability.

The following sub-groups of mutations are also interesting
(i.e. phytases comprising at least one mutation selected from
either one of the groups of):

E58A, D69K, D197N, T214L, E222T, E267D, R291I, R329H,
25 S364T, A379K, G404A;

F54Y, I73V, K94A, R101A, N153K, V158I, A203G, S205G,
V217A, A227V, V234L, P238A, Q277E, A287H, A292Q, V366I, A396S,
E415Q, G437A, R451E;

E58A, D69K, D197N, F54Y, I73V, K94A;
30 T214L, E222T, E267DR101A, N153K, V158I;
R291I, R329H, S364TA203G, S205G, V217A;

A379K, G404AA227V, V234L, P238A, Q277E;
A287H, A292Q, V366I, A396S, E415Q, G437A, R451E;
T214L, E222T, S364T, V158I, A203G, G404A, A227V, P238A,
A396S, G437A, R451E.

5 Examples of host cells are plant cells, animal cells, and microbial cells, e.g. prokaryotic or eukaryotic cells, such as bacterial, fungal or yeast cells. An example of a fungal host is a strain of the genus *Aspergillus*, and examples of yeast hosts are strains of *Saccharomyces*, and strains of *Hansenula*.

10 The invention also relates to a modified protein obtainable or obtained by any of the processes described above.

 The invention also relates to a variant or mutein of a phytase such as (but not limited to) the consensus phytase-1, wherein, in the amino acid sequence in Figure 2, at least one
15 of the following replacements have been effected: Q50L, Q50T, Q50G, Q50T-Y51N, Q50L-Y51N or Q50T-K91A.

 In the third aspect mentioned above, a consensus sequence is determined from homologous sequences as described above; in a second step the active center of the protein comprising all
20 amino acid residues that are involved in forming the active center is determined in the consensus sequence and in the sequence of a single homologous protein as well. The single homologous protein may have preferred properties like high specific activity or different pH dependency of enzymatic
25 activity. In a third step some or all amino acid residues that are involved in forming the active center of the homologous protein are inserted into the backbone of the consensus sequence. The result thereof is a chimeric protein having the active center derived from a single protein and the backbone of
30 the consensus sequence.

The active center of the protein can be determined e.g. by using any analysis of the three-dimensional structure of the protein, e.g. by homology modelling on the basis of a known 3D-structure of a known protein.

5 The present invention also provides consensus proteins obtainable or obtained by such processes, in particular proteins comprising at least one of the amino acid sequences shown in Figures 2-6, 10 or 21, or variants or muteins thereof. Examples of such variants are shown in Figs. 7-9.

10 Such variants or muteins can be defined and prepared on the basis of the teachings given in European Patent Application number 0897010, e.g. Q50L, Q50T, Q50G, Q50L-Y51N, or Q50T-Y51N. These mutations are defined as above, or, alternatively, by reference to Fig. 2. When referring to Fig. 2, no subtraction of
15 the 26 amino acid signal peptide is required (e.g. in "Q50L," at position 50 of the amino acid sequence of Fig. 2, the amino acid Q has been replaced by amino acid L).

A food, feed, or pharmaceutical composition comprising the phytases of the invention is another aspect of the invention.

20 In this context, and relating to the process of the invention, "at least three, preferably at least four amino acid sequences of such defined protein family" means that three, four, five, six to twelve, twenty, fifty, or even more sequences can be used for the alignment and the comparison to create the
25 amino acid sequence of the consensus protein. "Sequences of a defined protein family" means that such sequences fold into a three-dimensional structure, wherein the alpha-helices, the beta-sheets and beta-turns are at the same position so that such structures are, as called by the man skilled in the art, largely
30 superimposable. Furthermore these sequences characterize proteins that show the same type of biological activity, e.g. a

defined enzyme class, e.g. the phytases. The three-dimensional structure of one such protein is sufficient to allow the modelling of the structure of the other homologous proteins of such a family. An example, how this can be done, is given in

5 Example 1. "Evolutionary similarity" in the context of the present invention refers to a scheme which classifies amino acids regarding their structural similarity which allows that one amino acid can be replaced by another amino acid with a minimal influence on the overall structure, as this is done e.g.

10 by programs, like "PRETTY", known in the art. The phrase "the degree of similarity provided by such a program...is set to less stringent number" means in the context of the present invention that values for the parameters which determine the degree of similarity in the program used in the practice of the present

15 invention are chosen in a way to allow the program to define a consensus amino acid for a maximum of positions of the whole amino acid sequence, e. g. in case of the program PRETTY a value of 2 or 3 for the THRESHOLD and a value of 2 for the PLURALITY can be chosen. Furthermore, "a vote weight of one divided by the

20 number of such sequences" means in the context of the present invention that the sequences which define a group of sequences with a higher degree of similarity as the other sequences used for the determination of the consensus sequence only contribute to such determination with a factor which is equal to one

25 divided by the number of all sequences of this group.

As mentioned before, should the program not allow to select the consensus amino acid, the most frequent amino acid is selected; should the latter be impossible the man skilled in the art will select an amino acid from all the sequences used for

30 the comparison which is known in the art for its property to improve the thermostability in proteins as discussed e.g. by

Janecek, S. (1993), *Process Biochem.* 28, 435-445; Fersht, A. R. & Serrano, L. (1993), *Curr. Opin. Struct. Biol.* 3, 75-83; Alber, T. (1989), *Annu. Rev. Biochem.* 58, 765-798; Matthews, B. W. (1987), *Biochemistry* 26, 6885-6888; or Matthews, B. W. (1991),
5 *Curr. Opin. Struct. Biol.* 1, 17-21.

The stability of an enzyme is relevant for many industrial applications. Therefore, a lot of attempts, more or less successful, have been made to improve the stability, preferably the thermostability of enzymes by rational or random approaches.

10 Here we present an alternative way to improve the thermostability of a protein.

The invention provides a process for the preparation of a consensus protein comprising a process to calculate an amino acid residue for nearly all positions of a so-called consensus
15 protein and to synthesize a complete gene from this sequence that can be expressed in a pro- or eukaryotic expression system.

DNA sequences of the present invention can be constructed starting from genomic or cDNA sequences encoding the proteins, e.g. phytases, of interest. For example, they can be constructed
20 by methods of in vitro mutagenesis [see e.g. Sambrook et al., *Molecular Cloning*, Cold Spring Harbor Laboratory Press, New York]. A widely used strategy for "site-directed mutagenesis", as originally outlined by Hurchinson and Edgell [*J. Virol.* 8, 181 (1971)], involves the annealing of a synthetic
25 oligonucleotide carrying the desired nucleotide substitution to a target region of a single-stranded DNA sequence wherein the mutation should be introduced [for review see Smith, *Annu. Rev. Genet.* 19, 423 (1985), and for improved methods, see references 2-6 in Stanssen et al., *Nucl. Acids Res.*, 17, 4441-4454 (1989).
30 Another possibility of mutating a given DNA sequence is the mutagenesis by using the polymerase chain reaction (PCR). DNA as

starting material can be isolated by methods known in the art and described e.g. in Sambrook et al. (Molecular Cloning) from the respective strains.

For strain information, see e.g. EP 684313 or any
5 depository authority indicated below. *Aspergillus niger* [ATCC 9142], *Myceliophthora thermophila* [ATCC 48102], *Talaromyces thermophilus* [ATCC 20186] and *Aspergillus fumigatus* [ATCC 34625] have been redeposited according to the conditions of the Budapest Treaty at the American Type Culture Cell Collection
10 under the following accession numbers: ATCC 74337, ATCC 74340, ATCC 74338 and ATCC 74339, respectively. It is, however, understood that DNA encoding a consensus protein in accordance with the present invention can also be prepared in a synthetic manner as described, e.g. in EP 747483 or EP 897985, or in the
15 examples, by methods known in the art.

For sequence information, see e.g. EP 684313, or sequence data bases, for example like Genbank (Intelligenetics, California, USA), European Bioinformatics Institute (Hinxton Hall, Cambridge, GB), NBRF (Georgetown University, Medical
20 Centre, Washington DC, USA) and Vecbase (University of Wisconsin, Biotechnology Centre, Madison, Wisconsin, USA).

The process of the present invention can e.g. be used to improve the thermostability of the enzyme phytase.

Once complete DNA sequences of the present invention have
25 been obtained they can be integrated into vectors by methods known in the art and described e.g. in Sambrook et al. (s.a.) to overexpress the encoded polypeptide in appropriate host systems. However, a man skilled in the art knows that also the DNA sequences themselves can be used to transform the suitable host
30 systems of the invention to get overexpression of the encoded polypeptide. Appropriate host systems are for example fungi,

like Aspergilli, e.g. *Aspergillus niger* [ATCC 9142] or *Aspergillus ficum* [NRRL 3135] or like *Trichoderma*, e.g. *Trichoderma reesei*; or yeasts, like *Saccharomyces*, e.g. *Saccharomyces cerevisiae* or *Pichia*, like *Pichia pastoris*, or
5 *Hansenula polymorpha*, e.g. *H. polymorpha* (DSM5215); or plants, as described, e.g. by Pen et al., *Bio/Technology* 11, 811-814 (1994). A man skilled in the art knows that such microorganisms are available from depository authorities, e.g. the American Type Culture Collection (ATCC), the Centraalbureau voor
10 Schimmelcultures (CBS) or the Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH (DSM) or any other depository authority as listed in the Journal "Industrial Property" [(1991) 1, pages 29-40]. Bacteria which can be used are e.g. *E. coli*; Bacilli as, e.g., *Bacillus subtilis*; or
15 *Streptomyces*, e.g. *Streptomyces lividans* (see e.g. Anné and Mallaert in *FEMS Microbiol. Lett.* 114, 121 (1993). Preferred *E. coli* strains, which can be used are *E. coli* K12 strains e.g. M15 [described as DZ 291 by Villarejo et al. in *J. Bacteriol.* 120, 466-474 (1974)], HB 101 [ATCC No. 33694] or *E. coli* SG13009
20 [Gottesman et al., *J. Bacteriol.* 148, 265-273 (1981)].

Vectors which can be used for expression in fungi are known in the art and described e.g. in EP 420358, or by Cullen et al. [*Bio/Technology* 5, 369-376 (1987)], Ward [*Molecular Industrial Mycology, Systems and Applications for Filamentous*
25 *Fungi*, Marcel Dekker, New York (1991)], Upshall et al. [*Bio/Technology* 5, 1301-1304 (1987)], Gwynne et al. [*Bio/Technology* 5, 71-79 (1987)], or Punt et al. [*J. Biotechnol.* 17, 19-34 (1991)]; and for yeasts by Sreekrishna et al. [*J. Basic Microbiol.* 28, 265-278 (1988), *Biochemistry* 28, 4117-4125
30 (1989)], Hitzemann et al. [*Nature* 293, 717-722 (1981)] or in EP 183070, EP 183071, EP 248227, or EP 263311. Suitable vectors

which can be used for expression in *E. coli* are mentioned, e.g. by Sambrook et al. [s.a.], Fiers et al. [Proc. 8th Int. Biotechnology Symposium", Soc. Franc. de Microbiol., Paris (Durand et al., eds.), pp. 680-697 (1988)], Bujard et al. [Meth. 5 Enzymol. 155, 416-433 (1987)], or Stüber et al. [Immunological Methods, eds. Lefkovits and Pernis, Academic Press, Inc., Vol. IV, 121-152 (1990)]. Vectors that can be used for expression in *Bacilli* are known in the art and described, e.g. in EP 207459, EP 405370, Proc. Natl. Acad. Sci. USA 81, 439 (1984) or Yansura 10 and Henner, Meth. Enzymol. 185, 199-228 (1990). Vectors which can be used for the expression in *H. Polymorpha* are known in the art and described, e.g. in Gellissen et al., Biotechnology 9, 291-295 (1991).

Either such vectors already carry regulatory elements, 15 e.g. promoters, or the DNA sequences of the present invention can be engineered to contain such elements. Suitable promotor elements which can be used are known in the art and are, e.g. for *Trichoderma reesei* the *cbh1*- [Haarki et al., Biotechnology 7, 596-600 (1989)] or the *pk11*-promotor [Schindler et al., Gene 20 130, 271-275 (1993)]; for *Aspergillus oryzae* the *amy*-promotor [Christensen et al., Abstr. 19th Lunteren Lectures on Molecular Genetics F23 (1987), Christensen et al., Biotechnology 6, 1419-1422 (1988), Tada et al., Mol. Gen. Genet. 229, 301 (1991)]; and for *Aspergillus niger* the *glaA*- [Cullen et al., Bio/Technology 25 5, 369-376 (1987), Gwynne et al., Bio/Technology 5, 713-719 (1987), Ward in Molecular Industrial Mycology, Systems and Applications for Filamentous Fungi, Marcel Dekker, New York, 83-106 (1991)], *alcA*- [Gwynne et al., Bio/Technology 5, 718-719 (1987)], *suc1*- [Boddy et al., Curr. Genet. 24, 60-66 (1993)], 30 *aphA*- [MacRae et al., Gene 71, 339-348 (1988), MacRae et al., Gene 132, 193-198 (1993)], *tpiA*- [McKnight et al., Cell 46, 143-

147 (1986), Upshall et al., Bio/Technology 5, 1301-1304 (1987)],
gpdA- [Punt et al., Gene 69, 49-57 (1988), Punt et al., J.
Biotechnol. 17, 19-37 (1991)] and the pkiA-promotor [de Graaff
et al., Curr. Genet. 22, 21-27 (1992)]. Suitable promotor
5 elements that can be used for expression in yeast are known in
the art and are, e.g. the pho5-promotor [Vogel et al., Mol.
Cell. Biol., 2050-2057 (1989); Rudolf and Hinnen, Proc. Natl.
Acad. Sci. 84, 1340-1344 (1987)] or the gap-promotor for
expression in *Saccharomyces cerevisiae*; the aox1-promotor [Koutz
10 et al., Yeast 5, 167-177 (1989); Sreekrishna et al., J. Basic
Microbiol. 28, 265-278 (1988)] for *Pichia pastoris*; or the FMD
promoter [Hollenberg et al., EPA No. 0299108] or MOX-promotor
[Ledeboer et al., Nucl. Acids Res. 13, 3063-3082 (1985)] for *H.*
polymorpha.

15 Accordingly vectors comprising DNA sequences of the
present invention, preferably for the expression of said DNA
sequences in bacteria or a fungal or a yeast host and such
transformed bacteria or fungal or yeast hosts are also a part of
the invention.

20 The invention also provides a system that allows for high
expression of proteins, in particular of the phytases of the
invention, such as recombinant *Hansenula* strains. To achieve
that, the codons of the DNA sequence of such a protein may be
selected on the basis of a codon frequency table of the organism
25 used for expression, e.g. of yeast as in the present case (see
e.g. in Example 1). Optionally, the codons for the signal
sequence may be selected in a manner as described for the
specific case in Example 1; that means that a codon frequency
table is prepared on the basis of the codons used in the DNA
30 sequences which encode the amino acid sequences of the given
protein family. Then the codons for the design of the DNA

sequence of the signal sequence are selected from a codon frequency table of the host cell used for expression whereby always codons of comparable frequency in both tables are used.

Once such DNA sequences have been expressed in an appropriate host cell in a suitable medium, the encoded protein can be isolated either from the medium in the case the protein is secreted into the medium or from the host organism in case such protein is present intracellularly by methods known in the art of protein purification or described in case of a phytase, e.g. in EP 420358. Accordingly, a process for the preparation of a polypeptide of the present invention wherein transformed bacteria or a host cell as described above are cultured under suitable culture conditions, and the polypeptide is recovered therefrom and a polypeptide when produced by such a process; or a polypeptide encoded by a DNA sequence of the present invention, are also a part of the present invention.

Once obtained, the polypeptides of the present invention can be characterized regarding their properties that make them useful in agriculture by any assay known in the art.

In general, the polypeptides of the present invention can be used without being limited to a specific field of application, e.g. in case of phytases for the conversion of inositol polyphosphates, like phytate, to inositol and inorganic phosphate.

Furthermore, the polypeptides of the present invention can be used in a process for the preparation of a pharmaceutical composition or compound food or feeds wherein the components of such a composition are mixed with at least one polypeptide of the present invention. Accordingly, compound food or feeds or pharmaceutical compositions comprising at least one polypeptide of the present invention are also a part of the present

invention. A man skilled in the art is familiar with their process of preparation. Such pharmaceutical compositions or compound foods or feeds can further comprise additives or components generally used for such purpose and known in the
5 state of the art.

The present invention also provides a process for the reduction of levels of phytate in animal manure wherein an animal is fed such a feed composition in an amount effective in converting phytate contained in the feedstuff to lower inositol
10 phosphates and/or inositol, and inorganic phosphate.

In the present context, a phytase is an enzyme or polypeptide that has phytase activity. A phytase can be e.g. a myo-inositol hexakisphosphate phosphohydrolase, such as (myo-inositol hexakisphosphate 3-phosphohydrolase, EC 3.1.3.8) and
15 (myo-inositol hexakisphosphate 6-phosphohydrolase, EC 3.1.3.26).

In one embodiment, the phytase is purified, viz. at least 85%, preferably at least 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% pure, as evaluated by SDS-PAGE. The phytase may be isolated. Phytase activity can be determined using any
20 phytase assay known in the art, e.g. the assay described herein (see Example 9). The assay temperature may be the optimum temperature of the actual phytase, and the assay pH may be the optimum pH of the actual phytase.

The assay temperature may e.g. be selected within the
25 range of 20-90°C, or 30-80°C, or 35-75°C, for instance temperatures of 37°C, 50°C, 60°C, or 70°C.

The assay pH may e.g. be selected within the range of pH 2-9, or 3-8, or 3-6, for instance assay pH values of 3, 4, 5, 6, or 7 may be chosen.

30 Amino acid sequence homology (or polypeptide or amino acid homology) is determined as the degree of identity between two

sequences. This may suitably be determined by means of computer programs known in the art such as GAP provided in the GCG program package [Program Manual for the Wisconsin Package, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin 53711, USA], see also Needleman, S.B. and Wunsch, C.D., (1970), J. Mol. Biol., 48, 443-453]. In release 9.1, for comparing polypeptide sequences, the Length Weight is set to 0, and the Gap Weight is set to 3.0.

The degree of identity or homology between two DNA (nucleic acid) sequences may be determined by means of computer programs known in the art such as GAP provided in the GCG program package [Program Manual for the Wisconsin Package, Genetics Computer Group, 575 Science Drive, Madison, Wisconsin 53711, USA], see also Needleman, S.B. and Wunsch, C.D., (1970), J. Mol. Biol., 48, 443-453]. In release 9.1, GAP is used with the following settings for DNA sequence comparison: GAP creation penalty of 50 and GAP extension penalty of 3.

Suitable experimental conditions for determining whether a given DNA or RNA sequence hybridizes to a specified nucleotide or oligonucleotide probe involves presoaking of the filter containing the DNA or RNA fragments to examine for hybridization in 5 x SSC (Sodium chloride/Sodium citrate; (J. Sambrook, E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning, A Laboratory Manual, 2nd edition, Cold Spring Harbor, New York) for 10 min, and prehybridization of the filter in a solution of 5 x SSC, 5 x Denhardt's solution, 0.5 % SDS and 100 µg/ml of denatured sonicated salmon sperm DNA (Sambrook et al. 1989), followed by hybridization in the same solution containing a concentration of 10 ng/ml of a random-primed (Feinberg, A. P. and Vogelstein, B. (1983) Anal. Biochem. 132:6-13), ³²P-dCTP-labeled (specific

activity $> 1 \times 10^9$ cpm/ μ g) probe for 12 hours at approximately 45°C.

The filter is then washed twice for 30 minutes in 2 x SSC, 0.5 % SDS at at least 55°C (low stringency), at at least 60°C (medium stringency), at at least 65°C (medium/high stringency), at at least 70°C (high stringency), or at at least 75°C (very high stringency).

Molecules to which the oligonucleotide probe hybridizes under these conditions can be detected using an x-ray film.

10 Phytases of amended thermostability, or thermostable phytases, are one aspect of the present invention. A "thermostable" phytase is a phytase that has a T_m (melting temperature) - as measured on purified phytase protein by Differential Scanning Calorimetry (DSC) - of at least 65°C. For 15 the DSC, a constant heating rate may be used, e.g. of 10°C/min. In alternative embodiments, the T_m is at least 66, 67, 68, 69, 70, 71, 72, 73, 74 or 75°C. Or, the T_m is equal to or lower than 150°C, or equal to or lower than 145, 140, 135, 130, 125, 120, 115 or 110°C. Accordingly, examples of intervals of T_m are: 65- 20 150°C, 66-150°C, - (etc.) - 75-150°C; 65-145°C, 66-145°C, - (etc.) - 75-145°C; 65-140°C, - (etc.) - 75-140°C; - (etc.) - 65-110°C, 66-110°C, - (etc.) - 75-110°C.

Particular ranges for T_m are the following: between 65 and 110°C; between 70 and 110°C; between 70 and 100°C; between 75 25 and 95°C, or between 80 and 90°C.

In Examples 9 and 10 below, the measurement of T_m by DSC is described, and the T_m 's of a number of phytases are shown.

The optimum temperatures are also indicated, since - as an alternative mean - a thermostable phytase can be defined as a 30 phytase having a temperature-optimum of at least 60°C. Preferably, the optimum temperature is determined on the

substrate phytate or phytic acid at pH 5.0 or 5.5. Example 9 describes an example of a phytase assay, including a definition of units.

In alternative embodiments, the optimum temperature is at least 61, 62, 63, 64, 65, 66, 67, 68, 69 or 70°C. In a particular embodiment, the optimum temperature is equal to or lower than 140°C, or equal to or lower than 135, 130, 125, 120, 115, 110, 105 or 100°C. Accordingly, examples of intervals of optimum temperature are: 60-140°C, 61-140°C, - (etc.) - 70-140°C; 60-135°C, 61-135°C, - (etc.) - 70-135°C; 60-130°C, - (etc.) - 70-130°C; - (etc.) - 60-100°C, 61-100°C, - (etc.) - 70-100°C.

Before describing the present invention in more detail a short explanation of the Figures enclosed is given below.

15

Figure 1: Design of the consensus phytase-1 sequence. The letters represent the amino acid residues in the one-letter code. The following sequences were used for the alignment: phyA from *Aspergillus terreus* 9A-1 [Mitchell, D. B., Vogel, K., Weimann, B. J., Pasamontes, L. & van Loon, A. P. G. M. (1997) The phytase subfamily of histidine acid phosphatases: isolation of genes for two novel phytases from the fungi *Aspergillus terreus* and *Myceliophthora thermophila*, *Microbiology* 143, 245-252); from amino acid (aa) 27; SEQ ID NO: 1]; phyA from *A. terreus* cbs116.46 [EP 897985]. A heat resistant phytase of *Aspergillus fumigatus* with superior performance in animal experiments. Phytase optimization and natural variability. In: *The Biochemistry of phytate and phytases* (eds. Rasmussen, S.K; Raboy, V.; Dalbøge, H. and Loewus, F.; Kluwer Academic Publishers); from aa 27; SEQ ID NO: 2; phyA from *Aspergillus niger* var. *awamori* (Piddington et al (1993) *Gene* 133, 55-62;

from aa 27; SEQ ID NO: 3); phyA from *A. niger* T213 (EP 897985);
from aa 27; SEQ ID NO: 4); phyA from *A. niger* strain NRRL3135
[van Hartingsveldt, W., van Zeijl, C. M. F., Hartevelde, G. M.,
Gouka, R. J., Suykerbuyk, M. E. G., Luiten, R. G. M., van
5 Paridon, P. A., Selten, G. C. M., Veenstra, A. E., van Gorcom,
R. F. M., & van den Hondel, C. A. M. J. J. (1993) Cloning,
characterization and overexpression of the phytase-encoding gene
(phyA) of *Aspergillus niger*. *Gene* 127, 87-94; from aa 27; SEQ ID
NO: 5]; phyA from *Aspergillus fumigatus* ATCC 13073 (Pasamontes,
10 L., Haiker, M., Wyss, M., Tessier, M. & van Loon, A. P. G. M.
(1997) Cloning, purification and characterization of a heat
stable phytase from the fungus *Aspergillus fumigatus*, *Appl.*
Environ. Microbiol. 63, 1696-1700; from aa 25; SEQ ID NO: 6];
phyA from *A. fumigatus* ATCC 32722 (EP 897985); from aa 27; SEQ
15 ID NO: 7); phyA from *A. fumigatus* ATCC 58128 (EP 897985); from
aa 27; SEQ ID NO: 8); phyA from *A. fumigatus* ATCC 26906
(EP 897985); from aa 27; SEQ ID NO: 9); phyA from *A. fumigatus*
ATCC 32239 (EP 897985); from aa 30; SEQ ID NO: 10; phyA from
Emericella nidulans [Pasamontes, L., Haiker, M., Henriquez-
20 Huecas, M., Mitchell, D. B. & van Loon, A. P. G. M. (1997a).
Cloning of the phytases from *Emericella nidulans* and the
thermophilic fungus *Talaromyces thermophilus*. *Biochim. Biophys.*
Acta 1353, 217-223; from aa 25; SEQ ID NO: 11]; phyA from
Talaromyces thermophilus (Pasamontes et al., 1997a; from aa 24;
25 SEQ ID NO: 12); and phyA from *Myceliophthora thermophila*
(Mitchell et al., 1997; from aa 19; SEQ ID NO: 13). The
alignment was calculated using the program PILEUP. The location
of the gaps was refined by hand. Capitalized amino acid residues
in the alignment at a given position belong to the amino acid
30 coalition that establish the consensus residue. In bold, beneath
the calculated consensus sequence, the amino acid sequence of

the finally constructed consensus phytase (Fcp) is shown (SEQ ID NO: 14). The gaps in the calculated consensus sequence were filled by hand according to principals stated in Example 1.

5 Figure 2: DNA sequence (SEQ ID NO: 15) of the consensus phytase-1 gene (fcp) and of the primers used for the gene construction. The calculated amino acid sequence (Figure 1, SEQ ID NO: 14) was converted into a DNA sequence using the program BACKTRANSLATE [Devereux, J., Haeberli, P. & Smithies, O. (1984)
10 A comprehensive set of sequence analysis programs for the VAX. Nucl. Acids Res. 12, 387-395], and the codon frequency table of highly expressed yeast genes (GCG program package, 9.0). The signal peptide of the phytase from *A. terreus* cbs 116.46 was fused to the N-terminus. The amino acid sequence shown in Fig. 2
15 is SEQ ID NO: 16. The bold bases represent the sequences of the oligonucleotides used to generate the gene. The names of the respective oligonucleotides are alternately noted above or below the sequence. The underlined bases represent the start and stop codon of the gene. The bases written in italics represent the
20 two introduced Eco RI sites.

Figure 3: Alignment and consensus sequence of five Basidiomycete phytases. The letters represent the amino acid residues in the one-letter code. The amino acid sequences of the
25 phytases from *Paxillus involutus*, phyA1 (from aa 21; SEQ ID NO: 17; and phyA2 (from aa 21, WO 98/28409; SEQ ID NO: 18); *Trametes pubescens* (from aa 24, WO 98/28409; SEQ ID NO: 19); *Agrocybe pediades* (from aa 19, WO 98/28409; SEQ ID NO: 20); and *Peniophora lycii* (from aa 21, WO 98/28409; SEQ ID NO: 21),
30 starting with the amino acid residues mentioned in parentheses, were used for the alignment and the calculation of the

corresponding consensus sequence called "Basidio" (Example 2; SEQ ID NO: 22). The alignment was performed with the program PILEPUP. The location of the gaps was refined by hand. The consensus sequence was calculated by the program PRETTY. While a
5 vote weight of 0.5 was assigned to the two *P. involutus* phytases, all other genes were used with a vote weight of 1.0 for the consensus sequence calculation. At positions where the program was not able to determine a consensus residue, the Basidio sequence contains a dash. Capitalized amino acid
10 residues in the alignment at a given position represent the amino acid coalition that established the consensus residue.

Figure 4: Design of consensus phytase-10 amino acid sequence. By adding the sequence of *Thermomyces lanuginosus*
15 phytase [Berka, R. M., Rey, M. W., Brown, K. M., Byun, T. & Klotz, A. V. (1998) Molecular characterization and expression of a phytase gene from the thermophilic fungus *Thermomyces lanuginosus*. Appl. Environ. Microbiol. 64, 4423-4427; SEQ ID NO: 23] and the consensus sequence of the phytases from five
20 Basidiomycetes (SEQ ID NO: 22) to the alignment of Figure 1, an improved consensus sequence was calculated by the program PRETTY. Additionally, the amino acid sequence of *A. niger* T213 was omitted, and a vote weight of 0.5 was assigned to the remaining two *A. niger* phytase sequences. For further
25 information see Example 2.

Figure 5: DNA and amino acid sequence of consensus phytase-10 (SEQ ID NO: 25, and SEQ ID NO: 26, respectively). The amino acid sequence is written above the corresponding DNA
30 sequence using the one-letter code. The sequence of the oligonucleotides that were used to assemble the gene are in

bold letters. The names of the respective oligonucleotides and the amino acids that differ relative to consensus phytase-1 are underlined. The fcp10 gene was assembled from the following oligonucleotides: CP-1, CP-2, CP-3.10, CP-4.10, CP-5.10, CP-6, 5 CP-7.10, CP-8.10, CP-9.10, CP-10.10, CP-11.10, CP-12.10, CP-13.10, CP-14.10, CP-15.10, CP-16.10, CP-17.10, CP18.10, CP-19.10, CP-20.10, CP-21.10, and CP-22.10. The newly synthesized oligonucleotides are additionally marked by the number 10. The phytase contains the following 32 exchanges relative to 10 consensus phytase-1: Y54F, E58A, D69K, D70G, A94K, N134Q, I158V, S187A, Q188N, D197N, S204A, T214L, D220E, L234V, A238P, D246H, T251N, Y259N, E267D, E277Q, A283D, R291I, A320V, R329H, S364T, I366V, A379K, S396A, G404A, Q415E, A437G, A463E. The underlined mutations revealed a stabilizing effect on consensus phytase-1 15 when tested as single mutations in consensus phytase-1.

Figure 6: Alignment for the design of consensus phytase-11 (SEQ ID NO: 27). In contrast to the design of consensus phytase-10, for the design of the amino acid sequence of consensus 20 phytase-11, all Basidiomycete phytases were used as independent sequences using an assigned vote weight of 0.2 for each Basidiomycete sequence. Additionally, the amino acid sequence of *A. niger* T213 was again used in this alignment.

25 Figure 7: DNA and amino acid sequence of consensus phytase-1-thermo[8]-Q50T-K91A (SEQ ID NO: 28, and SEQ ID NO: 29, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to consensus phytase-1) 30 are underlined. The stop codon of the gene is marked by a star (*).

Figure 8: DNA and amino acid sequence of consensus phytase-10-thermo[3]-Q50T-K91A (SEQ ID NO: 30, and SEQ ID NO: 31, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to consensus phytase-10) are underlined. The stop codon of the gene is marked by a star (*).

10 Figure 9: DNA and amino acid sequence of *A. fumigatus* ATCC 13073 phytase alpha-mutant Q51T (SEQ ID NO: 32, and SEQ ID NO: 33, respectively). The amino acid sequence is written above the corresponding DNA sequence using the one-letter code. The replaced amino acid residues (relative to *A. fumigatus* ATCC 13073 phytase) are underlined. The stop codon of the gene is marked by a star (*).

Figure 10: DNA and amino acid sequence of consensus phytase-7 (SEQ ID NO: 34, and SEQ ID NO: 35, respectively). The amino acids are written above the corresponding DNA sequence using the one-letter code. The sequence of the oligonucleotides used to assemble the gene are in bold letters. Oligonucleotides and amino acids that were exchanged (relative to consensus phytase-1) are underlined and the corresponding triplets are written in small case letters. The fcp7 gene was assembled from the following oligonucleotides: CP-1, CP-2, CP-3, CP-4.7, CP-5.7, CP-6, CP-7, CP-8.7, CP-9, CP-10.7, CP-11.7, CP-12.7, CP-13.7, CP-14.7, CP-15.7, CP-16, CP-17.7, CP-18.7, CP-19.7, CP-20, CP-21, and CP-22. The newly synthesized oligonucleotides are additionally marked by the number 7. Consensus phytase-7 contains the following 24 exchanges in comparison to the

original consensus phytase-1: S89D, S92G, A94K, D164S, P201S, G203A, G205S, H212P, G224A, D226T, E255T, D256E, V258T, P265S, Q292H, G300K, Y305H, A314T, S364G, M365I, A397S, S398A, G404A, and A405S.

5

Figure 11: Differential scanning calorimetry (DSC) of consensus phytase-1 and consensus phytase-10. The protein samples were concentrated to about 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of consensus phytase-10 (upper graph) yielded a melting temperature of 85.4°C, which is 7.3°C higher than the melting point of consensus phytase-1 (78.1°C, lower graph).

15 Figure 12: Differential scanning calorimetry (DSC) of consensus phytase-10-thermo[3]-Q50T and consensus phytase-10-thermo[3]-Q50T-K91A. The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of consensus phytase-10-thermo[3]-Q50T (upper graph) yielded a melting temperature of 88.6°C, while the melting temperature of consensus phytase-10-thermo-Q50T-K91A was determined to be 89.3°C.

25 Figure 13: Comparison of the temperature optimum between consensus phytase-1, consensus phytase-10 and consensus phytase-10-thermo[3]-Q50T. For the determination of the temperature optimum, the phytase standard assay of Example 9 was performed at a series of temperatures between 37 and 86°C. The diluted supernatant of transformed *S. cerevisiae* strains was used for the determination. The other components of the supernatant had

no influence on the determination of the temperature optimum: \wedge , consensus phytase-1; \diamond , consensus phytase-10; \blacksquare , consensus phytase 10-thermo[3]-Q50T.

5 Figure 14: pH-dependent activity profile and substrate specificity of consensus phytase-10 and its variants thermo[3]-Q50T and thermo[3]-Q50T-K91A. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows the pH-
 10 dependent activity profile of consensus phytase-10 (\square), consensus phytase-10-thermo[3]-Q50T (\bullet), and consensus phytase-10-thermo[3]-Q50T-K91A (\wedge). Graph b) shows the corresponding substrate specificity tested by replacement of phytate in the standard assay by the indicated compounds; open bars, consensus
 15 phytase-10; grey bars, consensus phytase-10-thermo[3]-Q50T; dark bars, consensus phytase-10-thermo[3]-Q50T-K91A). The numbers correspond to the following substrates: 1, phytate; 2, p-nitrophenyl phosphate; 3, phenyl phosphate; 4, fructose-1,6-bisphosphate; 5, fructose-6-phosphate; 6, glucose-6-phosphate;
 20 7, ribose-5-phosphate; 8, DL-glycerol-3-phosphate; 9, glycerol-2-phosphate; 10, 3-phosphoglycerate; 11, phosphoenolpyruvate; 12, AMP; 13, ADP; 14, ATP.

Figure 15: pH-dependent activity profile and substrate
 25 specificity of consensus phytase-1-thermo[8]-Q50T and of consensus phytase-1-thermo[8]-Q50T-K91A. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows the pH-dependent activity profile of the Q50T- (\blacksquare) and the Q50T-K91A-

variant (.). Graph b) shows the corresponding substrate specificities tested by replacement of phytate in the standard assay by the indicated compounds (open bars, consensus phytase-1-thermo[8]-Q50T; filled bars, consensus phytase-1-thermo[8]-Q50T-K91A). The substrates are listed in the legend of Figure 14.

Figure 16: Differential scanning calorimetry (DSC) of consensus phytase-1-thermo[8]-Q50T and consensus phytase-1-thermo[8]-Q50T-K91A. The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of consensus phytase-1-thermo[8]-Q50T (upper graph) showed a melting temperature of 84.7°C, while the melting point of consensus phytase-1-thermo[8]-Q50T-K91A was found at 85.7°C.

Figure 17: Comparison of the temperature optimum between consensus phytase-1, consensus phytase-1-thermo[3] and consensus phytase-1-thermo[8]. For the determination of the temperature optimum, the phytase standard assay was performed at a series of temperatures between 37 and 86°C. Protein purified from the supernatant of transformed *S. cerevisiae* strains was used for the determination. O, consensus phytase-1; □, consensus phytase-1-thermo[3]; ▲, consensus phytase 1-thermo[8].

Figure 18: Comparison of the pH-dependent activity profile and substrate specificity between consensus phytase-1, consensus phytase-7, and the phytase from *A. niger* NRRL 3135. The phytase activity was determined using the standard assay in appropriate buffers (see Example 9) at different pH-values. Graph a) shows

the pH-dependent activity profile of consensus phytase-1 (■), the phytase from *A. niger* NRRL 3135 (○), and of consensus phytase-7 (▲). Graph b) shows the corresponding substrate specificities tested by replacement of phytate in the standard assay by the indicated compounds (black bars, *A. niger* NRRL 3135 phytase; open bars, consensus phytase-1; dashed bars, consensus phytase-7). The substrates are listed in the legend of Figure 14.

10 Figure 19: Differential scanning calorimetry (DSC) of the phytase from *A. fumigatus* ATCC 13073 and of its stabilized alpha-mutant, which contains the following amino acid exchanges: F55Y, V100I, F114Y, A243L, S265P, and N294D.

The protein samples were concentrated to ca. 50-60 mg/ml and extensively dialyzed against 10 mM sodium acetate, pH 5.0. A constant heating rate of 10°C/min was applied up to 95°C. DSC of *A. fumigatus* 13073 phytase (lower graph) revealed a melting temperature of 62.5°C, while the melting point of the alpha-mutant was found at 67.0°C.

20

Figure 20: Comparison of the temperature optima of *A. fumigatus* 13073 wild-type phytase, its alpha-mutant, and a further stabilized alpha-mutant (E59A-S154N-R329H-S364T-G404A). For the determination of the temperature optimum, the phytase standard assay was performed at a series of temperatures between 25 37 and 75°C. The diluted supernatant of transformed *S. cerevisiae* strains was used for the determination. The other components of the supernatant had no influence on the determination of the temperature optimum. ○, *A. fumigatus* ATCC 30 13073 phytase; ▲, *A. fumigatus* ATCC 13073 alpha-mutant; □, *A.*

fumigatus ATCC 13073 alpha-mutant-(E59A-S154N-R329H-S364T-G404A)-Q27T; ■, A. fumigatus ATCC 13073 alpha-mutant-(E59A-S154N-R329H-S364T-G404A)-Q51T-K92A. Q51T and K92A correspond to consensus phytase-1 substitutions Q50T and K91A, respectively.

5

Figure 21: Amino acid sequence of consensus phytase-12 (consphy12; SEQ ID NO: 36) which contains a number of active site residues transferred from the "basidio" consensus sequence to consensus phytase-10-thermo[3]-Q50T-K91A (underlined).

10

Figure 22: DNA and amino acid sequence of consensus phytase-3-thermo[11]-Q50T. The amino acids are written below the corresponding DNA sequence using the one-letter code.

15

Figure 23: DNA and amino acid sequence of consensus phytase-3-thermo[11]-Q50T-K91A. The amino acids are written below the corresponding DNA sequence using the one-letter code.

Figure 24: DNA and amino acid sequence of consensus phytase-10-thermo[5]-Q50T. The amino acids are written below the corresponding DNA sequence using the one-letter code.

Figure 25: DNA and amino acid sequence of consensus phytase-10-thermo[5]-Q50T-K91A. The amino acids are written below the corresponding DNA sequence using the one-letter code.

The phytase-producing microorganism strains mentioned herein, viz. Paxillus involutus CBS 100231; Peniophora lycii CBS 686.96; Agrocybe pediades CBS 900.96; and Trametes pubescens CBS 100232; were isolated from natural samples originating from, respectively, Denmark; Denmark; Denmark; and Sweden (the Uppsala

collection. The samples were collected in November 1992; October 1993; June 1995; and in November 1995, respectively.

Example 1

5 Consensus phytase-1

The amino acid sequence of consensus phytase-1 (fungal consensus phytase, fcp) was designed and calculated as described in Examples 1 and 2 of EP 897985. Table 1 below shows the origin and vote weight of the phytase amino acid sequences used for the
10 design of consensus phytase-1. The consensus phytase-1 sequence was furthermore converted into a DNA sequence as described in Example 3 of EP 897985, and the consensus phytase-1 gene was constructed and cloned as described in Example 4 of EP 897985.

15 Table 1

Origin and vote weight of the phytase amino acid sequences

- phyA from *Aspergillus terreus* 9A-1, aa 27, vote weight 0.5 (Mitchell et al., 1997)
- phyA from *Aspergillus terreus* cbs116.46, aa 27, vote weight
20 0.5 (EP 897985)
- phyA from *Aspergillus niger* var. *awamori*, aa 27, vote weight 0.33 [Piddington, C. S., Houston, C. S., Paloheimo, M., Cantrell, M., Miettinen-Oinonen, A., Nevalainen, H., & Rambosek, J. (1993) The cloning and sequencing of the genes encoding
25 phytase (phy) and pH 2.5-optimum acid phosphatase (aph) from *Aspergillus niger* var. *awamori*. Gene 133, 55-62].
- phyA from *Aspergillus niger* T213 (EP 897985), aa 27, vote weight 0.33
- 30 - phyA from *Aspergillus niger* strain NRRL3135, aa 27, vote weight 0.33 (van Hartingsveldt et al., 1993)

- phyA from *Aspergillus fumigatus* ATCC 13073, aa 26, vote weight 0.2 (Pasamontes et al., 1997)
- phyA from *Aspergillus fumigatus* ATCC 32722, aa 26, vote weight 0.2 (EP 897985)
- 5 - phyA from *Aspergillus fumigatus* ATCC 58128, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 26906, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 32239, aa 30, vote weight
10 0.2 (EP 897985)
- phyA from *Emmericella nidulans* , aa 25, vote weight 1.0 (Pasamontes et al., 1997a)
- phyA from *Talaromyces thermophilus* ATCC 20186, aa 24, vote weight 1.0 (Pasamontes et al., 1997a)
- 15 - phyA from *Myceliophthora thermophila*, aa 19, vote weight 1.0 (Mitchell et al., 1997)

Example 2

Design of an improved consensus phytase (consensus 20 phytase-10) amino acid sequence

The alignments used for the design of consensus phytase-10 were calculated using the program PILEUP from the GCG Sequence Analysis Package Release 9.0 (Devereux et al., 1984) with the
25 standard parameters (gap creation penalty 12, gap extension penalty 4). The location of the gaps was refined using a text editor.

The following sequences were used for the alignment of the Basidiomycete phytases starting with the amino acid (aa)
30 mentioned in Table 2:

Table 2

Origin and vote weight of five Basidiomycete phytases used for the calculation of the corresponding consensus amino acid sequence (basidio)

5

- phyA1 from *Paxillus involutus* CBS No. 100231, aa 21, vote weight 0.5 (WO 98/28409)

- phyA2 from *Paxillus involutus* CBS No. 100231, aa 21, vote weight 0.5 (WO 98/28409)

10 - phyA from *Trametes pubescens* CBS No. 100232, aa 24, vote weight 1.0 (WO 98/28409)

- phyA from *Agrocybe pediades* CBS No. 900.96, aa 19, vote weight 1.0 (WO 98/28409)

- phyA from *Peniophora lycii* CBS No. 686.96, aa 21, vote weight 1.0 (WO 98/28409)

The alignment is shown in Figure 3.

In Table 3 the genes that were used for the final alignment are listed. The first amino acid (aa) of the sequence that is used in the alignment is mentioned behind the organism's designation.

Table 3

25 Origin and vote weight of the phytase sequences used for the design of consensus phytase-10

- phyA from *Aspergillus terreus* 9A-1, aa 27, vote weight 0.5 (Mitchell et al., 1997)

30 - phyA from *Aspergillus terreus* cbs116.46, aa 27, vote weight 0.5 (EP 897985)

- phyA from *Aspergillus niger* var. *awamori*, aa 27, vote weight 0.5 (Piddington et al., 1993)
- phyA from *Aspergillus niger* strain NRRL3135, aa 27, vote weight 0.5 (van Hartingsveldt et al., 1993)
- 5 - phyA from *Aspergillus fumigatus* ATCC 13073, aa 26, vote weight 0.2 (Pasamontes et al., 1997)
- phyA from *Aspergillus fumigatus* ATCC 32722, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 58128, aa 26, vote weight 10 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 26906, aa 26, vote weight 0.2 (EP 897985)
- phyA from *Aspergillus fumigatus* ATCC 32239, aa 30, vote weight 0.2 (EP 897985)
- 15 - phyA from *Emmericella nidulans* , aa 25, vote weight 1.0 (Pasamontes et al., 1997a)
- phyA from *Talaromyces thermophilus* ATCC 20186, aa 24, vote weight 1.0 (Pasamontes et al., 1997a)
- phyA from *Myceliophthora thermophila*, aa 19, vote weight 1.0 20 (Mitchell et al., 1997)
- phyA from *Thermomyces lanuginosus*, aa 36, vote weight 1.0 (Berka et al., 1998)
- Consensus sequence of five Basidiomycete phytases, vote weight 1.0 (Basidio, Figure 3)

25

The corresponding alignment is shown in Figure 4.

Calculation of the amino acid sequence of consensus
phytase-10

30 To improve the alignment, we added the original consensus
sequence of five phytases from four different Basidiomycetes

(called Basidio; still containing the undefined sequence positions; see Figure 3), nearly all phytase sequences used for the calculation of the original consensus phytase sequences and one new phytase sequence from the Ascomycete *Thermomyces* 5 *lanuginosus* to a larger alignment.

We set plurality on 2.0 and threshold on 3. The used vote weights are listed in Table 3. The alignment and the corresponding consensus sequence are presented in Figure 4. The new consensus phytase sequence has 32 different amino acids in 10 comparison to the original consensus phytase-1. Positions for which the program PRETTY was not able to calculate a consensus amino acid residue were filled according to rules mentioned in Example 1. None of the residues suggested by the program was replaced.

15 Furthermore, in another calculation, we included all Basidiomycete phytases as single amino acid sequences but assigning a vote weight of 0.2 in the calculation. The corresponding alignment is shown in Figure 6. The calculated consensus amino acid sequence (consensus phytase-11) has the 20 following differences to the sequence of consensus phytase-10. Letter X means that the program was not able to calculate a consensus amino acid; the amino acid in parenthesis corresponds to the amino acid finally included into consensus phytase-10.

D35X (first letter for consensus phytase-10, last letter 25 for consensus phytase-11), X(K)69K, X(E)100E, A101R, Q134N, X(K)153N, X(H)190H, X(A)204S, X(E)220D, E222T, V227A, X(R)271R, H287A, X(D)288D, X(K)379K, X(I)389I, E390X, X(E)415E, X(A)416A, X(R)446L, E463A. The numbering is as in Fig. 5.

We also checked single amino acid replacements suggested 30 by the improved consensus sequences 10 and 11 on their influence

on the stability of the original consensus phytase-1. The approach is described in example 3.

Conversion of the consensus phytase-10 amino acid sequence
5 into a DNA sequence

The first 26 amino acid residues of *A. terreus* cbs116.46 phytase were used as signal peptide and fused to the N-terminus of consensus phytase-10. The used procedure is further described in Example 1.

10 The resulting sequence of the fcp10 gene is shown in Figure 5.

Construction and cloning of the consensus phytase-10 gene
(fcp10)

15 The calculated DNA sequence of fcp10 was divided into oligonucleotides of 85 bp, alternately using the sequence of the sense and the anti-sense strand. Every oligonucleotide overlaps 20 bp with the previous and the following oligonucleotide of the opposite strand. The location of all primers, purchased from
20 Microsynth, Balgach (Switzerland) and obtained in a PAGE-purified form, is indicated in Figure 5.

PCR-Reactions

In three PCR reactions, the synthesized oligonucleotides
25 were composed to the entire gene. For the PCR, the High Fidelity Kit from Boehringer Mannheim (Boehringer Mannheim, Mannheim, Germany) and the thermo cycler "The ProtokollTM" from AMS Biotechnology (Europe) Ltd. (Lugano, Switzerland) were used. The following oligonucleotides were used in a concentration of 0.2
30 pMol/ml.

Mix 1.10: CP-1, CP-2, CP-3.10, CP-4.10, CP-5.10, CP-6,
CP-7.10, CP-8.10, CP-9.10, CP-10.10

5 Mix 2.10: CP-9.10, CP-11.10, CP-12.10, CP-13.10, CP-
14.10, CP-15.10, CP-16.10, CP-17.10, CP18.10,
CP-19.10, CP-20.10, CP-21.10, CP-22.10

The newly synthesized oligonucleotides are marked by the
number 10. Consensus phytase-10 contains the following 32
exchanges, which are underlined in Figure 5, in comparison to
10 the original consensus phytase-1: Y54F, E58A, D69K, D70G, A94K,
N134Q, I158V, S187A, Q188N, D197N, S204A, T214L, D220E, L234V,
A238P, D246H, T251N, Y259N, E267D, E277Q, A283D, R291I, A320V,
R329H, S364T, I366V, A379K, S396A, G404A, Q415E, A437G, A463E.

Four short PCR primers were used for the assembling of the
15 oligonucleotides:

CP-a: *Eco RI*

5'-TATATGAATTCATGGGCGTGTTCGTC-3' (SEQ ID NO: 37)

20 CP-b:

5'-TGAAAAGTTCATTGAAGGTTTC-3' (SEQ ID NO: 38)

CP-c.10:

5'-TCTTCGAAAGCAGTACACAAAC-3' (SEQ ID NO: 39)

25

CP-e: *Eco RI*

5'-TATATGAATTCCTTAAGCGAAAC-3' (SEQ ID NO: 40)

PCR reaction a: 10 μ l Mix 1.10 (2.0 pmol of each
oligonucleotide)
2 μ l nucleotides (10 mM of each nucleotide)
2 μ l primer CP-a (10 pmol/ml)
5 2 μ l primer CP-c.10 (10 pmol/ml)
10,0 μ l PCR buffer
0.75 μ l polymerase mixture (2.6 U)
73.25 μ l H₂O

10 PCR reaction b: 10 μ l Mix 2.10 (2.0 pmol of each
oligonucleotide)
2 μ l nucleotides (10 mM each nucleotide)
2 μ l primer CP-b (10 pmol/ml)
2 μ l primer CP-e (10 pmol/ml)
15 10,0 μ l PCR buffer
0.75 μ l polymerase mixture (2.6 U)
73.25 μ l H₂O

Reaction conditions for PCR reactions a and b:

20 step 1 2 min - 45°C
step 2 30 sec - 72°C
step 3 30 sec - 94°C
step 4 30 sec - 52°C
step 5 1 min - 72°C

25

Steps 3 to 5 were repeated 40-times.

The PCR products (670 and 905 bp) were purified by agarose
gel electrophoresis (0.9% agarose), followed by gel extraction
30 (QIAEX II Gel Extraction Kit, Qiagen, Hilden, Germany). The
purified DNA fragments were used for the PCR reaction c.

PCR reaction c: 6 μ l PCR product of reaction a \approx 50 ng)
6 μ l PCR product of reaction b \approx 50 ng)
2 μ l primer CP-a (10 pmol/ml)
5 2 μ l primer CP-e (10 pmol/ml)
10,0 μ l PCR buffer
0.75 μ l polymerase mixture (2.6 U)
73.25 μ l H₂O

10 Reaction conditions for PCR reaction c:

step 1 2 min - 94°C
step 2 30 sec - 94°C
step 3 30 sec - 55°C
step 4 1 min - 72°C

15

Steps 2 to 4 were repeated 31-times.

The resulting PCR product (1.4 kb) was purified as mentioned above, digested with EcoRI, and ligated in an EcoRI-
20 digested and dephosphorylated pBsk(-)-vector (Stratagene, La Jolla, CA, USA). 1 μ l of the ligation mixture was used to transform E. coli XL-1 competent cells (Stratagene, La Jolla, CA, USA). All standard procedures were carried out as described by Sambrook et al. (1987). The DNA sequence of the constructed
25 gene (fcp10) was checked by sequencing as known in the art.

Example 3

Increasing the thermostability of consensus phytase-1 by
introduction of single mutations suggested by the amino
acid sequences of consensus phytase-10 and consensus
phytase-11

5

In order to increase the thermostability of homologous genes, it is also possible to test the stability effect of each differing amino acid residue between the protein of interest and the calculated consensus sequence and to combine all stabilizing mutations into the protein of interest. We used the consensus phytase-1 as protein of interest and tested the effect on the protein stability of 34 amino acid residues that differ relative to consensus phytase-10 and/or -11 by single site-directed mutagenesis.

15

To construct muteins for expression in *A. niger*, *S. cerevisiae*, or *H. polymorpha*, the corresponding expression plasmid containing the consensus phytase-1 gene was used as template for site-directed mutagenesis (see Examples 6-8). Mutations were introduced using the "quick exchange™ site-directed mutagenesis kit" from Stratagene (La Jolla, CA, USA) following the manufacturer's protocol and using the corresponding primers. All mutations made and the corresponding primers are summarized in Table 4. Plasmids harboring the desired mutation were identified by DNA sequence analysis as known in the art.

20

25

Table 4Primers used for site-directed mutagenesis of consensus phytase-
1

Exchanged bases are highlighted in bold. The introduction of a
5 restriction site is marked above the sequence. When a
restriction site is written in parenthesis, the mentioned site
was destroyed by introduction of the mutation.

mutation	Primer set
	<i>Kpn I</i>
10 Q50T	5'-CACTTGTGGGGT ACCT ACTCTCCATACTTCTC-3' (SEQ ID NO: 41) 5'-GAGAAGTATGGAGAGTAG GT ACCCCAAGTG-3'
Y54F	5'-GGTCAATACTCTCCATTCT TT CTCTTTGGAAG-3' (SEQ ID NO: 42)
15 5'-CTTCCAAAGAGAAG AA TGGAGAGTATTGACC-3'	
E58A	5'-CATACTTCTCTTTGGCAGACGAATCTGC-3' (SEQ ID NO: 43) 5'-GCAGATTCGTCTGCCAAAGAGAAGTATG-3'
	<i>Aat II</i>
20 D69K	5'-CTCCAGACGT CCCA AAGGACTGTAGAGTTAC-3' (SEQ ID NO: 44) 5'-GTAACCTCTACAGTC CTTT GGGACGTCTGGAG-3'
	<i>Aat II</i>
25 D70G	5'-CTCCAGACGT CCCA GACGGCTGTAGAGTTAC-3' (SEQ ID NO: 45) 5'-GTAACCTCTACAGCCGTCTGG G ACGTCTGGAG-3'
K91A	5'-GATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTG-3' (SEQ ID NO: 46)
30 5'-CAGAGTAAGCCTTAGAC GC AGAAGAAGTTGGGTATC-3'	
	<i>Sca I</i>
A94K	5'-CTTCTAAGTCTAAG AA GTACTCTGCTTTG-3' (SEQ ID NO: 47) 5'-CAAAGCAGAGTACT TT CTTAGACTTAGAAG-3'
35 A101R	5'-GCTTACTCTGCTTTGATTGAAC CG GATTCAAAGAACGCTAC-3' (SEQ ID NO: 48) 5'-GTAGCGTTCTTTTGAAT CC GTTCAATCAAAGCAGAGTAAGC-3'
40 N134Q	5'-CCATTGGGTGAACAGCAAATGGTTAACTC-3' (SEQ ID NO: 49) 5'-GAGTTAACCATTTGCTGTTACCGAATGG-3'

- Nru I*
- K153N 5'-GATACAAGGCTCTCGCGAGAAACATTGTTC-3' (SEQ ID NO: 50)
5'-GGAACAATGTTTCTCGCGAGAGCCTTGTATC-3'
- Bss HI*
- 5 I158V 5'-GATTGTTCCATTCTGTCGCGCTTCTGGTTC-3' (SEQ ID NO: 51)
5'-GAACCAGAAGCGCGCACGAATGGAACAATC-3'
- Apa I*
- 10 S187A 5'-GGCTGACCCAGGGGCCAACCACACCAAGC-3' (SEQ ID NO: 53)
5'-GCTTGGTGTGGTTGGGCCCTGGGTCAGCC-3'
- Bcl I*
- 15 D197N 5'-CTCCAGTTATTAACGTGATCATTCCAGAAGG-3' (SEQ ID NO: 52)
5'-CCTTCTGGAATGATCACGTTAATAACTGGAG-3'
- Nco I*
- 20 T214L 5'-CACTTTGGACCATGGTCTTTGTAAGTCTTTCG-3' (SEQ ID NO: 54)
5'-CGAAAGCAGTACAAAGACCATGGTCCAAAGTG-3'
- Avr II*
- E222T 5'-GCTTTCGAAGACTCTACCCTAGGTGACGACGTTG-3' (SEQ ID NO: 55)
5'-CAACGTCGTCACCTAGGGTAGAGTCTTCGAAAGC-3'
- 25 V227A 5'-GGTGACGACGCTGAAGCTAACTTCAC-3' (SEQ ID NO: 56)
5'-GTGAAGTTAGCTTCAGCGTCGTCACC-3'
- Sac II*
- 30 L234V 5'-CTAACTTCACCGCGGTGTTTCGCTCCAG-3' (SEQ ID NO: 57)
5'-CTGGAGCGAACACCGCGGTGAAGTTAG-3'
- A238P 5'-GCTTTGTTTCGCTCCACCTATTAGAGCTAGATTGG-3' (SEQ ID NO: 58)
35 5'-CCAATCTAGCTCTAATAGGTGGAGCGAACAAAGC-3'
- Hpa I*
- T251N 5'-GCCAGGTGTTAACTTGACTGACGAAG-3' (SEQ ID NO: 59)
40 5'-TTCGTCAGTCAAGTTAACACCTGGC-3'
- Aat II*
- Y259N 5'-GACGAAGACGTCGTTAACTTGATGGAC-3' (SEQ ID NO: 60)
5'-GTCCATCAAGTTAACGACGTCTTCGTC-3'
- Asp I*
- 45 E267D 5'-GTCCATTTCGACACTGTCGCTAGAACTTC-3' (SEQ ID NO: 61)
5'-GAAGTTCTAGCGACAGTGTCGAATGGAC-3'

E277Q 5' -CTGACGCTACTCAGCTGTCTCCATTC-3' (SEQ ID NO: 62)
5' -GAATGGAGACAGCTGAGTAGCGTCAG-3'

5 A283D 5' -GTCTCCATTCTGTGATTTGTTCACTCAC-3' (SEQ ID NO: 63)
5' -GTGAGTGAACAAATCACAGAATGGAGAC-3'

Ksp I

10 H287A 5' -GCTTTGTTCA**CCGCGG**ACGAATGGAG-3' (SEQ ID NO: 64)
5' -CTCCATTCGT**CCGCGG**TGAACAAAGC-3'

Bam HI

15 R291I 5' -CACGACGAATGGAT**CCA**TACGACTAC-3' (SEQ ID NO: 65)
5' -GTAGTCGTATT**GGATC**CAATTCGTCGTG-3'

Bsi WI

Q292A 5' -GACGAATGGAGAG**CGTAC**GACTACTTG-3' (SEQ ID NO: 66)
5' -CAAGTAGTC**GTACG**CTCTCCATTCGTC-3'

Hpa I

20 A320V 5' -GGTGGTTGGTTTC**GT**TAACGAATTGATTGC-3' (SEQ ID NO: 67)
5' -GCAATCAATTC**GT**TA**AC**GAAACCAACACC-3'

(Bgl II)

25 R329H 5' -GCTAGATTGACT**CACTC**TCCAGTTCAAG-3' (SEQ ID NO: 68)
5' -CTTGAACTGGAGAG**GTGAGT**CAATCTAGC-3'

Eco RV

30 S364T 5' -CTCACGACAACACTATGAT**AT**TCTATTTTCTTC-3' (SEQ ID NO: 69)
5' -GAAGAAAATAGAT**AT**TCATAGTGTTCGTGAG-3'

Nco I

35 I366V 5' -CGACAACT**CCATG**TTTCTATTTTCTTCGC-3' (SEQ ID NO: 70)
5' -GCGAAGAAAATAGAA**ACCATG**GAGTTGTCG-3'

Kpn I

A379K 5' -GTACAACGGTAC**CAAGC**ATTGTCTAC-3' (SEQ ID NO: 71)
5' -GTAGACAATGG**CTTG**GTAACCGTTGTAC-3'

40 S396A 5' -CTGACGGTTACGCTGCTTCTTGGAC-3' (SEQ ID NO: 72)
5' -GTCCAAGAAGCAGCGTAACCGTCAG-3'

G404A 5' -CTGTTCCATTCGCTGCTAGAGCTTAC-3' (SEQ ID NO: 73)
5' -GTAAGCTCTAGCAGCGAATGGAACAG-3'

45 Q415E 5' -GATGCAATGTGAAGCTGAAAAGGAACC-3' (SEQ ID NO: 74)
5' -GGTTCCTTTTCAGCTT**CAC**ATTGCATC-3'

Sal I

A437G 5'-CACGGTTGTGGTGT**CGACA**AGTTGGG-3' (SEQ ID NO: 75)
 5'-CCCAACTTGT**CGACACCACA**ACCGTG-3'

5

Mun I

A463E 5'-GATCTGGTGG**CAATT**GGGAGGAATGTTTCG-3' (SEQ ID NO: 76)
 5'-CGAAACATT**CCTCCCAATTG**CCACCAGATC-3'

10 and, accordingly, for other mutations.

The temperature optimum of the purified phytases, expressed in *Saccharomyces cerevisiae* (Example 7), was determined as outlined in Example 9. Table 5 shows the effect of
 15 each mutation introduced on the stability of consensus phytase-1.

Table 5

Stability effect of the individual amino acid replacements in
 20 consensus phytase-1

+ or - means a positive, respectively, negative effect on the protein stability up to 1°C, ++ and -- means a positive, respectively, negative effect on the protein stability between 1 and 3°C; the numbers 10 or 11 in parentheses indicate the
 25 consensus phytase sequence that suggested the amino acid replacement.

stabilizing		neutral		destabilizing	
mutation	effect	mutation	effect	mutation	effect
E58A (10)	+	D69A	±	Y54F (10)	-
D69K (11)	+	D70G (10)	±	V73I	-
D197N (10)	+	N134Q (10)	±	A94K (10)	-
T214L (10)	+ +	G186H	±	A101R (11)	-
E222T (11)	+ +	S187A (10)	±	K153N (11)	-
E267D (10)	+	T214V	±	I158V (10)	- -
R291I	+	T251N (10)	±	G203A	- -
R329H (10)	+	Y259N (10)	±	G205S	-
S364T (10)	+ +	A283D (10)	±	A217V	-
A379K (11)	+	A320V (10)	±	V227A (11)	- -
G404A (10)	+ +	K445T	±	L234V (10)	-
		A463E (10)	±	A238P (10)	- -
				E277Q (10)	-
				H287A (11)	-
				Q292A	-
				I366V (10)	-
				S396A (10)	- -
				Q415E (11)	-
				A437G (10)	- -
				E451R	- -

We combined eight positive mutations (E58A, D197N, E267D, R291I, R329H, S364T, A379K, G404A) in consensus phytase-1 thermo[8], using the primers and the technique mentioned above in this example. Furthermore, the mutations Q50T and/or K91A were introduced which mainly influence the catalytic characteristics of phytase (see patent applications EP 897010 and EP 897985, as well as Example 9). The DNA and amino acid sequence of the resulting phytase (consensus phytase-1 thermo[8]-Q50T-K91A) are shown in Figure 7. In this way, the temperature optimum and the melting point of the consensus phytase were increased by 7°C (Figures 15, 16, 17).

In a further consensus protein, we combined eleven positive mutations (E58A, D69K, D197N, T214L, E222T, E267D, R291I, R329H, S364T, A379K, G404A) in consensus phytase-1 thermo[11]. Furthermore, the mutations Q50T and/or K91A were

introduced. In this way, the melting temperature was increased by another 3-4°C when compared to consensus phytase-1 thermo[8].

Using the results of Table 5, we further improved the thermostability of consensus phytase-10 by the back mutations K94A, V158I, and A396S, the reverse of which (A94K, I158V, and S396A) revealed a strong negative influence on the stability of consensus phytase-1. The resulting protein was called consensus phytase-10-thermo[3]. SEQ ID NO: 26 plus the three mutations K94A, V158I, and A396S. Furthermore, we introduced the mutations Q50T and K91A that mainly influence the catalytic characteristics of consensus phytase (see patent applications EP 897010 and EP 897985, as well as Example 9 and Figures 14 and 15). The resulting DNA and amino acid sequence are shown in Figure 8. The optimized phytase showed a 4°C higher temperature optimum and melting point than consensus phytase-10 (Figures 12 and 13). Furthermore, the phytase has also a strongly increased specific activity with phytate as substrate of 250 U/mg at pH 5.5 (Figure 14).

In a still further consensus protein, two additional mutations were introduced into consensus phytase-10 thermo[3] (E222T, G437A) which yielded consensus phytase-10 thermo[5]. Furthermore, the mutations Q50T and/or K91A were introduced. In this way, the melting temperature was increased by another 1-2°C when compared to consensus phytase-10 thermo[3].

Example 4

Stabilization of the phytase of A. fumigatus ATCC 13073 by replacement of amino acid residues with the corresponding consensus phytase-1 and/or consensus phytase-10 residues

5

At six amino acid sequence positions where A. fumigatus 13073 phytase is the only or nearly the only phytase in the alignment of Figure 1 that does not contain the corresponding consensus phytase amino acid residue, the non-consensus amino acid residue was replaced by the consensus one. The following amino acids were substituted in A. fumigatus 13073 phytase, containing additionally the Q51(24)T substitution (influencing the catalytic properties and corresponding to the Q50T substitution in the consensus phytases) and the signal sequence of A. terreus cbs116.46 phytase (see European Patent Application No. 0897010, and Figure 9): F55(28)Y, V100(73)I, F114(87)Y, A243(220)L, S265(242)P, N294(282)D. The numbers in parentheses refer to the numbering in Figure 1.

In a second round, four of the seven stabilizing amino acid exchanges (E58A, R329H, S364T, G404A) identified in consensus phytase-10 and tested as single mutations in consensus phytase-1 (Table 5) were additionally introduced into the A. fumigatus alpha-mutant. Furthermore, the amino acid replacement S154N, shown to reduce the protease susceptibility of the phytase, was introduced.

The mutations were introduced as described in Example 3 (see Table 6) and expressed as described in Examples 6 to 8. The resulting A. fumigatus 13073 phytase variants were called alpha-mutant (i.e. the A. fumigatus ATCC 13073 phytase with the substitutions Q24T, F28Y, V73I, F87Y, A220L, S242P, N282D) and "optimized" alpha-mutant (i.e. the A. fumigatus alpha-mutant

having the additional substitutions E59A-S154N-R329H-S364T-G404A). K92A is an additional preferred mutation.

The temperature optimum (60°C, Figure 20) and the melting temperature (67.0°C, Figure 19) of the *A. fumigatus* 13073 alpha-
5 mutant phytase were increased by 5-7°C in comparison to the values of the wild-type phytase (temperature optimum: 55°C, T_m: 60°C). The five additional amino acid replacements further increased the temperature optimum by 3°C (Figure 20).

10 Table 6

Mutagenesis primers for the stabilization of *A. fumigatus* ATCC 13073 phytase

Mutation	Primer
15 F55Y	5'-CACGTACTCGCCATACTTTTCGCTCGAG-3' (SEQ ID NO: 77) 5'-CTCGAGCGAAAAGTATGGCGAGTACGTG-3'
	(Xho I)
E58A	5'-CCATACTTTTCGCTCGCGGACGAGCTGTCCGTG-3' (SEQ ID NO: 78)
20	5'-CACGGACAGCTCGTCCGCGAGCGAAAAGTAGG-3'
V100I	5'-GTATAAGAAGCTTATTACGGCGATCCAGGCC-3' (SEQ ID NO: 79)
25	5'-GGCCTGGATCGCCGTAATAAGCTTCTTATAC-3'
F114Y	5'-CTTCAAGGGCAAGTACGCCTTTTTGAAGACG-3' (SEQ ID NO: 80)
	5'-CGTCTTCAAAAAGGCGTACTTGCCCTTGAAG-3'
30	
A243L	5'-CATCCGAGCTCGCCTCGAGAAGCATCTTC-3' (SEQ ID NO: 81) 5'-GAAGATGCTTCTCGAGGCGAGCTCGGATG-3'
S265P	5'-CTAATGGA TGTGTCCGTTTGATACGGTAG-3' (SEQ ID NO: 82)
35	5'-CTACCGTATCAAACGGACACATGTCCATTAG-3'
N294D	5'-GTGGAAGAAGTACGACTACCTTCAGTC-3' (SEQ ID NO: 83) 5'-GACTGAAGGTAGTCGTACTTCTTCCAC-3'

(Mlu I)

R329H 5'-GCCCCGGTTGACGCAATTCGCCAGTGCAGG-3' (SEQ ID NO: 84)
 5'-CCTGCACTGGCGAATGCGTCAACCGGGC-3'

5

Nco I

S364T 5'-CACACGACAACACCATGGTTTCCATCTTC-3' (SEQ ID NO: 85)
 5'-GAAGATGGAAACCATGCTGTTGTCGTGTG-3'

(Bss HI)

10 G404A 5'-GTGGTGCCTTTCGCCGCGCGAGCCTACTTC-3' (SEQ ID NO: 86)
 5'-GAAGTAGGCTCGCGCGGCGAAAGGCACCAC-3'

Example 5

Introduction of the active site amino acid residues of A.
 15 niger NRRL 3135 phytase into consensus phytase-1

We used the crystal structure of *Aspergillus niger* NRRL 3135 phytase to define all active site amino acid residues (see Example 1, and EP 897010). Using the alignment of Figure 1, we replaced the following active site residues and additionally
 20 the non-identical adjacent ones of consensus phytase-1 by those of A. niger phytase:

S89D, S92G, A94K, D164S, P201S, G203A, G205S, H212P, G224A, D226T, E255T, D256E, V258T, P265S, Q292H, G300K, Y305H, A314T, S364G, M365I, A397S, S398A, G404A, and A405S.

25 The new consensus phytase-7 protein sequence was backtranslated into a DNA sequence (Figure 10) as described in Example 1. The corresponding gene (fcp7) was generated as described in Example 1 using the following oligonucleotide mixes:

30 Mix 1.7: CP-1, CP-2, CP-3, CP-4.7, CP-5.7, CP-6, CP-7, CP-8.7, CP-9, CP-10.7

Mix 2.7: CP-9, CP-10.7, CP-11.7, CP-12.7, CP-13.7, CP-14.7, CP-15.7, CP-16, CP-17.7, CP-18.7, CP-19.7, CP-20,
 35 CP-21, CP-22.

The DNA sequences of the oligonucleotides are indicated in Figure 10. The newly synthesized oligonucleotides are additionally marked by the number 7. After assembling of the 5 oligonucleotides using the same PCR primers as mentioned in Example 1, the gene was cloned into an expression vector as described in Examples 6-8.

The pH-profile of the enzyme determined after expression in *H. polymorpha* and purification was very similar to that of *A. niger* phytase (see Figure 18).

Example 6

Expression of the consensus phytase genes in *Hansenula polymorpha*

15 The phytase expression vectors used to transform *H. polymorpha* RB11 [Gellissen, G., Hollenberg, C. P., Janowicz, Z. A. (1994) Gene expression in methylotrophic yeasts, in Smith, A. (ed.) Gene expression in recombinant microorganisms. Dekker, New York, pp. 395-439] were constructed by inserting the Eco RI fragment 20 of pBsk-fcp or variants thereof into the multiple cloning site of the *H. polymorpha* expression vector pFPMT121, which is based on an *ura3* selection marker from *S. cerevisiae*, a formate dehydrogenase (FMD) promoter element and a methanol oxidase (MO) terminator element from *H. polymorpha*. The 5' end of the fcp 25 gene is fused to the FMD promoter, the 3' end to the MOX terminator (Gellissen et al., Appl. Microbiol. Biotechnol. 46, 46-54, 1996; EP 299108). The resulting expression vectors are designated pFPMTfcp, pFPMTfcp10, and pFPMTfcp7.

The constructed plasmids were propagated in *E. coli*. 30 Plasmid DNA was purified using standard state of the art procedures. The expression plasmids were transformed into the *H.*

polymorpha strain RB11 deficient in orotidine-5'-phosphate decarboxylase (ura3) using the procedure for preparation of competent cells and for transformation of yeast as described in Gellissen et al. (1996). Each transformation mixture was plated
5 on YNB medium (0.14% w/v Difco YNB and 0.5% ammonium sulfate) containing 2% glucose and 1.8% agar, and incubated at 37 °C. After 4 to 5 days individual transformant colonies were picked and grown in the liquid medium described above for 2 days at 37 °C. Subsequently, an aliquot of this culture was used to
10 inoculate fresh vials with YNB-medium containing 2% glucose. After seven further passages in selective medium, the expression vector had integrated into the yeast genome in multimeric form. Subsequently, mitotically stable transformants were obtained by two additional cultivation steps in 3 ml non-selective liquid
15 medium (YPD, 2% glucose, 10 g/l yeast extract, and 20 g/l peptone). In order to obtain genetically homogeneous recombinant strains, an aliquot from the last stabilization culture was plated on a selective plate. Single colonies were isolated for analysis of phytase expression in YNB containing 2% glycerol
20 instead of glucose to derepress the FMD promoter. Purification of the consensus phytases was done as described in Example 7.

Example 7

Expression of the consensus phytase genes in Saccharomyces
25 cerevisiae and purification of the phytases from the
culture supernatant

The consensus phytase genes were isolated from the corresponding Bluescript-plasmid (pBsk-fcp, pBSK-fcp10, pBsk-
30 fcp7) and ligated into the Eco RI sites of the expression cassette of the Saccharomyces cerevisiae expression vector pYES2

(Invitrogen, San Diego, CA, USA) or subcloned between the shortened GAPFL (glyceraldehyde-3-phosphate dehydrogenase) promoter and the pho5 terminator as described by Janes et al., Curr. Genet. 18, 97-103. The correct orientation of the gene was
5 checked by PCR. Transformation of *S. cerevisiae* strains, e.g. INVSc1 (Invitrogen, San Diego, CA, USA), was done according to Hinnen et al., Proc. Natl. Acad. Sci. USA 75, 1929-1933 (1978). Single colonies harboring the phytase gene under the control of the GAPFL promoter were picked and cultivated in 5 ml selection
10 medium [SD-uracil; Sherman, J. P., Finck, G. R. & Hicks, J. B. (1986) Laboratory course manual for methods in yeast genetics. Cold Spring Harbor University] at 30°C under vigorous shaking (250 rpm) for one day. The preculture was then added to 500 ml YPD medium (Sherman et al., 1986) and grown under the same
15 conditions. Induction of the gal1 promoter was done according to the manufacturer's instructions. After four days of incubation, the cell broth was centrifuged (7000 rpm, GS3 rotor, 15 min, 5°C) to remove the cells, and the supernatant was concentrated by way of ultrafiltration in Amicon 8400 cells (PM30 membranes;
20 Grace AG, Wallizeller, Switzerland) and ultrafree-15 centrifugal filter devices (Biomax-30K, Millipore, Bedford, MA, USA). The concentrate (10 ml) was desalted on a 40 ml Sephadex G25 Superfine column (Pharmacia Biotech, Freiburg, Germany), with 10 mM sodium acetate, pH 5.0, serving as elution buffer. The
25 desalted sample was brought to 2 M $(\text{NH}_4)_2\text{SO}_4$ and directly loaded onto a 1 ml Butyl Sepharose 4 Fast Flow hydrophobic interaction chromatography column (Pharmacia Biotech, Feiburg, Germany) which was eluted with a linear gradient from 2 M to 0 M $(\text{NH}_4)_2\text{SO}_4$ in 10 mM sodium acetate, pH 5.0. Phytase was eluted in the
30 breakthrough, concentrated and loaded on a 120 ml Sephacryl S-300 gel permeation chromatography column (Pharmacia Biotech,

Freiburg, Germany). Consensus phytases -1, -7 and -10 eluted as a homogeneous symmetrical peak and were shown by SDS-PAGE to be approx. 95% pure.

5 Example 8

Expression of the consensus phytase genes in Aspergillus niger

 The Bluescript-plasmids pBsk-fcp, pBsk-fcp10, and pBsk-fcp7 were used as template for the introduction of a Bsp HI-site
10 upstream of the start codon of the genes and an Eco RV-site downstream of the stop codon. The ExpandTM High Fidelity PCR Kit (Boehringer Mannheim, Mannheim, Germany) was used with the following primers:

15 Primer Asp-1:

Bsp HI

 5'-TATATCATGAGCGTGTTCGTCGTGCTACTGTTC-3' (SEQ ID NO: 87)

Primer Asp-2 used for cloning of fcp and fcp7:

20

Eco RV

 3'-ACCCGACTTACAAAGCGAATTCTATAGATATAT-5' (SEQ ID NO: 88)

Primer Asp-3 used for cloning of fcp10:

25

Eco RV

 3'-ACCCTTCTTACAAAGCGAATTCTATAGATATAT-5' (SEQ ID NO: 89)

 The reaction was performed as described by the supplier.
30 The PCR-amplified fcp-genes had a new Bsp HI site at the start codon, introduced by primer Asp-1, which resulted in a

replacement of the second amino acid residue glycine by serine. Subsequently, the DNA-fragment was digested with Bsp HI and Eco RV and ligated into the Nco I site downstream of the glucoamylase promoter of *Aspergillus niger* (glaA) and the Eco RV site upstream of the *Aspergillus nidulans* tryptophan C terminator (trpC) (Mullaney et al., 1985). After this cloning step, the genes were sequenced to detect possible errors introduced by PCR. The resulting expression plasmids, which basically correspond to the pGLAC vector as described in Example 9 of EP 684313, contained the orotidine-5'-phosphate decarboxylase gene (pyr4) of *Neurospora crassa* as a selection marker. Transformation of *Aspergillus niger* and expression of the consensus phytase genes was done as described in EP 684313. The consensus phytases were purified as described in Example 7.

Example 9

Determination of phytase activity and of the pH and temperature optima

This example relates i.a. to the determination of phytase activity and of the temperature optimum. Various phytases have been tested.

The phytase of *Aspergillus niger* NRRL 3135 was prepared as described in EP 420358 and by van Hartingsveldt et al. (Gene 127, 87-94, 1993).

The phytases of *Aspergillus fumigatus* ATCC 13073, *Aspergillus terreus* 9A-1, *Aspergillus terreus* cbs116.46, *Emericella nidulans*, *Myceliophthora thermophila*, and *Talaromyces thermophilus* were prepared as described in EP-0897985 and in the references therein.

The remaining phytases tested were prepared as described herein.

Consensus phytase-1-thermo(8) designates a variant of consensus phytase-1, which further comprises the eight mutations which are underlined in the legend to Figure 5. Consensus phytase-1 is shown in Fig. 1 (SEQ ID NO: 14) without signal peptide, and in Fig. 2 (SEQ ID NO: 16) with the signal peptide.

Phytase activity was determined basically as described by Mitchell et al. (1997). The activity was measured in an assay mixture containing 0.5% phytic acid (≈ 5 mM) in 200 mM sodium acetate, pH 5.0. After 15 min of incubation at 37°C, the reaction was stopped by addition of an equal volume of 15% trichloroacetic acid. The liberated inorganic phosphate was quantified by mixing 100 μ l of the assay mixture with 900 μ l H₂O and 1 ml of 0.6 M H₂SO₄, 2% ascorbic acid and 0.5% ammonium molybdate. Standard solutions of potassium phosphate were used as reference. One unit of enzyme activity was defined as the amount of enzyme that releases 1 μ mol phosphate per minute at 37°C. The protein concentration was determined using the enzyme extinction coefficient at 280 nm calculated according to Pace et al. [Pace N. C., Vajdos, F., Fee, L., Grimsley, G. & Gray, T. (1995) How to measure and predict the molar absorption coefficient of a protein. Prot. Sci. 4, 2411-2423]: 1 absorption unit (1 OD) at 280 nm corresponds to 1.101 mg/ml of consensus phytase-1, 1.068 mg/ml of consensus phytase-7, and 1.039 mg/ml of consensus phytase-10.

In case of pH-optimum curves, the purified enzymes were diluted in 10 mM sodium acetate, pH 5.0. Incubations were started by mixing aliquots of the diluted protein with an equal volume of 1% phytic acid (≈ 10 mM) in a series of different buffers: 0.4 M glycine/HCl, pH 2.5; 0.4 M acetate/NaOH, pH 3.0, 3.5, 4.0, 4.5, 5.0, 5.5; 0.4 M imidazole/HCl, pH 6.0, 6.5; 0.4 M Tris/HCl pH 7.0, 7.5, 8.0, 8.5, 9.0. Control experiments showed

that pH was only slightly affected by the mixing step. Incubations were performed for 15 min at 37°C as described above.

For determination of the substrate specificities of the 5 phytases, phytic acid in the assay mixture was replaced by 5 mM concentrations of the respective phosphate compounds. Besides, the activity tests were performed as described above.

For determination of the temperature optimum, enzyme (100 μ l) and substrate solution (100 μ l) were pre-incubated for 5 min 10 at the given temperature. The reaction was started by addition of the substrate solution to the enzyme. After 15 min of incubation, the reaction was stopped with trichloroacetic acid, and the amount of phosphate released was determined.

The pH-optimum of consensus phytase-1 was around pH 6.0- 15 6.5 (70 U/mg). Introduction of the Q50T mutation shifted the pH-optimum to pH 6.0 (130 U/mg). Introduction of the K91A mutation further shifted the pH optimum into the more acidic pH-range. Comparable effects of the Q50T and K91A mutations were also observed for consensus phytase-10 and for further 20 stabilized consensus phytase variants (Figures 14 and 15).

Consensus phytase-7, which was constructed to transfer the catalytic characteristics of *A. niger* NRRL 3135 phytase to consensus phytase-1, had a pH-profile very similar to that of *A. niger* NRRL 3135 phytase (see Figure 18). The substrate 25 specificity also resembled more that of *A. niger* NRRL 3135 phytase than that of consensus phytase-1.

The temperature optimum of consensus phytase-1 (71°C) was 16-26°C higher than the temperature optima of the wild-type phytases (45-55°C, Table 7) that were used to calculate the 30 consensus sequence. The improved consensus phytase-10 showed a further increase of its temperature optimum to 80°C (Figure 13).

The temperature optimum of consensus phytase-1-thermo[8] was found to be in the same range (78°C) when using the supernatant of an overproducing *S. cerevisiae* strain. The highest temperature optimum reached of 82°C was determined for consensus phytase-10-thermo[3]-Q50T-K91A. Table 7

Temperature optima and T_m-values of consensus phytase and of the phytases from *A. fumigatus*, *A. niger*, *E. nidulans*, and *M. thermophila*.

10

The determination of the temperature optimum was performed as described in Example 9. The T_m-values were determined by differential scanning calorimetry as described in Example 10.

Phytase	Optimum temperature (°C)	T _m (°C)
<i>Aspergillus niger</i> NRRL 3135	55	63.3
<i>Aspergillus fumigatus</i> ATCC 13073	55	62.5
<i>Aspergillus terreus</i> 9A-1	49	57.5
<i>Aspergillus terreus</i> cbs116.46	45	58.5
<i>Emericella nidulans</i>	45	55.7
<i>Myceliophthora thermophila</i>	55	-
<i>Talaromyces thermophilus</i>	45	-
Consensus phytase- 10-thermo[5]-Q50T- K91A	-	90.4
Consensus-phytase- 10-thermo[3]-Q50T- K91A	82	89.3

55

Consensus-phytase-10-thermo[3]-Q50T	82	88.6
Consensus-phytase-10	80	85.4
Consensus phytase-1-thermo[11]-Q50T-K91A	-	88.0
Consensus phytase-1-thermo[11]-Q50T	-	88.5
Consensus-phytase-1-thermo[8]-Q50T-K91A	-	85.7
Consensus-phytase-1-thermo[8]-Q50T	78	84.7
Consensus-phytase-1-thermo[8]	81	-
Consensus-phytase-1-thermo[3]	75	-
Consensus-phytase-1-Q50T	-	78.9
Consensus-phytase-1	71	78.1
Aspergillus fumigatus α -mutant Q51T	60	67.0
Aspergillus fumigatus α -mutant, plus mutations E59A, S154N, R329H, S364T, G404A	63	-
Aspergillus fumigatus "optimized" alpha-mutant, plus mutation K92A	63	-

Example 10Determination of the melting temperature by differential scanning calorimetry (DSC)

5 In order to determine the unfolding temperature of the phytases, differential scanning calorimetry was applied as described by Brugger et al., 1997 [Brugger, R., Mascarello, F., Augem, S., van Loon, A. P. G. M. & Wyss, M. (1997). Thermal denaturation of phytases and pH 2.5 acid phosphatase studied by
10 differential scanning calorimetry. In The Biochemistry of phytate and phytase (eds. Rasmussen, S.K.; Raboy, V.; Dalbøge, H. and Loewus, F.; Kluwer Academic Publishers, Dordrecht, the Netherlands]. Solutions of 50-60 mg/ml of homogeneous phytase were used for the tests. A constant heating rate of 10°C/min was ap-
15 plied up to 90-95°C.

The determined melting points confirm the results obtained for the temperature optima (Table 7). The most stable consensus phytase designed so far is consensus phytase-10-thermo[3]-Q50T-K91A showing a melting temperature under the chosen conditions
20 of 89.3°C. This is 26.0 to 33.6°C higher than the melting temperature of the wild-type phytases used.

Example 11Transfer of basidiomycete phytase active site into
25 consensus phytase-10-thermo[3]-Q50T-K91A

As described previously (Example 5), mutations derived from the basidiomycete phytase active sites were introduced into consensus phytase-10. The following five constructs a) to e) were prepared:

30 a) The construct called consensus phytase-12, and it comprises a selected number of active site residues of the

basidio consensus sequence. Its amino acid sequence is shown in Fig. 21 (the first 26 amino acids form the signal peptide; positions differing from consensus phytase-10-thermo[3]-Q50T-K91A are underlined);

5 b) a cluster of mutations (Cluster II) was transferred to the consensus phytase-1 and -10 sequences, viz.: S80Q, Y86F, S90G, K91A, S92A, K93T, A94R, Y95I;

 c) in a similar way, another cluster of mutations (Cluster III) was transferred, viz.: T129V, E133A, Q134N, M136S, V137S,
10 N138Q, S139A;

 d) in a similar way, a further cluster of mutations (Cluster IV) was transferred, viz.: A168D, E171T, K172N, F173W;

 e) and finally, a further cluster of mutations (Cluster V) was transferred, viz.: Q297G, S298D, G300D, Y305T.

15 These constructs were expressed as described in Examples 6 to 8.

Example 12

Phytase alignment using GAP

20 The phytases described herein - i.e. the amino acid sequences as well as the corresponding DNA sequences - were aligned against each other. Also some other phytases were correspondingly aligned, viz. the following:

- the consensus phytase-1 described in EP 897985;
- 25 - the phytase derived from *Aspergillus niger* (ficuum) NRRL 3135 (*A. niger* NRRL3135) described in EP 420358;
- the phytases derived from *Aspergillus fumigatus* ATCC 13073 (*A. fumigatus* 13073); *Aspergillus fumigatus* ATCC 32239 (*A. fumigatus* 32239); *Aspergillus terreus* cbs116.46 (*A. terreus* cbs);
- 30 *Emericella nidulans* (*E. nidulans*); and *Talaromyces thermophilus* (*T. thermophilus*) - all described in EP 897010;

- the phytases derived from *Myceliophthora thermophila* (*M. thermophila*); and *Aspergillus terreus* 9-A1 (*A. terreus* 9-A1) - both described in EP 684313;
- the phytase derived from *Thermomyces lanuginosus* (*T. lanuginosus*) described in WO 9735017 (PCT/US97/04559);
- the phytases derived from *Agrocybe pediades* (*A. pediades*), *Paxillus involutus* 1 and 2 (*P. involutus* phyA1 and phyA2); and *Trametes pubescens* (*T. pubescens*) - all described in WO 98/28409; and
- 10 - the phytase derived from *Peniophora lycii* (*P. lycii*) described in WO 98/28408.

For the alignments, the program GAP was used with the settings as described above.

For polypeptide comparisons, the signal peptides were
15 included with the exception of comparisons with consensus phytase-11.

The results of the amino acid sequence comparisons are shown in Table 8 below. The first number in each cell is the amino acid similarity, the second number is the amino acid
20 identity.

For DNA sequence comparisons, the signal sequence was always included. The results are shown in Table 9 below.

This invention comprises e.g. the following embodiments (A) to (J) that are described below.

25 In these embodiments, when determining % identity or % similarity at the amino acid level for another phytase, its amino acid sequence is aligned with the reference sequence (e.g. in embodiment (A) the consensus phytase-10 amino acid sequence), using an alignment program such as GAP referred to above.
30 Percentage identity, as well as percentage similarity, is

calculated by the program. The amino acid sequence of the other phytase may or may not include the signal peptide.

When determining % identity on the DNA level for another phytase-encoding DNA, this DNA sequence is aligned with the
5 reference sequence [e.g. in embodiment (A) nucleotides 12-1412 of SEQ ID NO: 25 (the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5], using an alignment program such as GAP referred to above. Percentage identity is calculated by the program. The DNA sequence encoding the other phytase can be a
10 genomic DNA sequence including introns, or it can be a cDNA sequence. It may or may not include the signal peptide-encoding part.

When determining hybridization, the probe to be used is the specified DNA sequence [e.g. in embodiment (A) nucleotides
15 12-1412 of SEQ ID NO: 25 (the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5)]. The DNA sequence encoding the other phytase can be a genomic DNA sample which contains a phytase-encoding DNA-sequence; a purified genomic DNA sequence (purified with respect to the phytase-encoding DNA sequence); or
20 it can be a phytase-encoding cDNA sequence, preferably purified or amplified, e.g. PCR-amplified. The phytase-encoding DNA, whatever type, may or may not include the signal peptide-encoding part. Suitable hybridization conditions are referred to above.

25 The term "DNA sequence" includes such fragments or parts of the herein exemplified DNA sequences, as long as they are capable of encoding an active enzyme (e.g. phytase).

The term "amino acid sequence" includes such fragments or parts of the herein exemplified amino acid sequences, as long
30 as they are enzymatically active (e.g. displaying phytase activity).

(A) Phytases and corresponding DNA sequences related to
consensus phytase-10 (CP10, Fcp 10)

A phytase that comprises an amino acid sequence which is at least 93.80%; or at least 94, 94.5, 95, 95.5, 96, 96.5, 97,
5 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10 (Fcp10) as shown in Fig. 5.

A phytase that comprises an amino acid sequence which is at least 95.09%; or at least 95.5, 96, 96.5, 97, 97.5, 98, 98.5,
99, 99.5% similar to the sequence of amino acids 1-467 of
10 consensus phytase-10.

A phytase which is encoded by a DNA sequence which is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99,
99.5% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 (Fcp10) as shown in Fig. 5.

15 A DNA sequence which encodes a phytase and which (i) is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 12-1412 of the DNA sequence of consensus phytase-10
20 (Fcp10) as shown in Fig. 5. A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP10, CP10-thermo[3]-Q50T, K91A, CP1-thermo[8], CP1-thermo[8]Q50T, K91A.

A DNA sequence which encodes a phytase comprising an amino
25 acid sequence which is at least 93.80%; or at least 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10 (Fcp10) as shown in Fig. 5.

(B) Phytases and corresponding DNA sequences related to consensus phytase-10-thermo[3]-Q50T-K91A

A phytase which comprises an amino acid sequence which is at least 93.37%; or at least 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 5 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A phytase which comprises an amino acid sequence which is at least 94.66%; or at least 95.0, 95.5, 96, 96.5, 97, 97.5, 98, 10 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A phytase which is encoded by a DNA sequence which is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 12-1412 of the DNA sequence of 15 consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

A DNA sequence which encodes a phytase and which (i) is at least 95.88%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to 20 nucleotides 12-1412 of the DNA sequence of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8. A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP10, CP10-thermo[3]-Q50T-K91A, CP1-thermo[8], or CP1-thermo[8]-Q50T-K91A.

25 A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 93.37%; or at least 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-10-thermo[3]-Q50T-K91A as shown in Fig. 8.

(C) Phytases and corresponding DNA sequences related to consensus phytase-1-thermo[8]

A phytase which comprises an amino acid sequence which is at least 98.30%; or at least 98.5, 99, 99.5% identical to the
5 sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

A phytase which comprises an amino acid sequence which is at least 98.51%; or at least 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown
10 in Fig. 7; backmutations T50Q and A91K to be added).

A phytase which is encoded by a DNA sequence which is at least 98.73%; or at least 99, 99.5% identical to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

15 A DNA sequence which encodes a phytase and which (i) is at least 98.73%; or at least 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8] (as shown in Fig. 7;
20 backmutations T50Q and A91K to be added). A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP1-thermo[8], CP1-thermo[8]-Q50T-K91A.

A DNA sequence which encodes a phytase comprising an amino
25 acid sequence which is at least 98.30%; or at least 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8] (as shown in Fig. 7; backmutations T50Q and A91K to be added).

(D) Phytases and corresponding DNA sequences related to
consensus phytase-1-thermo[8]-Q50T-K91A

A phytase which comprises an amino acid sequence which is at least 97.87%; or at least 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7.

A phytase which comprises an amino acid sequence which is at least 98.08%; or at least 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7.

A phytase which is encoded by a DNA sequence which is at least 98.37%; or at least 98.5, 99, 99.5% identical to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7.

A DNA sequence which encodes a phytase and which (i) is at least 98.37%; or at least 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1407 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A as shown in Fig. 7. A suitable negative control is DNA encoding consensus phytase-1. A suitable positive control is DNA encoding any of CP1-thermo[8], CP1-thermo[8]-Q50T-K91A.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 97.87%; or at least 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase 1-thermo[8]-Q50T-K91A as shown in Fig. 7.

(E) Phytases and corresponding DNA sequences related to
consensus phytase-11

A phytase that comprises an amino acid sequence which is at least 90.71%; or at least 91, 91.5, 92, 92.5, 93, 93.5, 94,

94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

A phytase that comprises an amino acid sequence which is at least 92.07%; or at least 92.5, 93, 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

A DNA sequence that encodes a phytase comprising an amino acid sequence which is at least 90.71%; or at least 91. 91.5, 92, 92.5, 93, 93.5, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-482 of consensus phytase-11 as shown in Fig. 6.

(F) Phytases and corresponding DNA sequences related to A. fumigatus alpha-mutant

A phytase that comprises an amino acid sequence which is at least 97.17%; or at least 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of A. fumigatus alpha-mutant (phytase) as shown in Fig. 9.

A phytase that comprises an amino acid sequence that is at least 97.82%; or at least 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of A. fumigatus alpha-mutant (phytase) as shown in Fig. 9.

A phytase which is encoded by a DNA sequence which is at least 96.13%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 1-1401 of the DNA sequence of A. fumigatus ATCC 13073 alpha-mutant (phytase) as shown in Fig. 9.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 97.17%; or at least 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467

of *A. fumigatus* ATCC 13073 alpha-mutant (phytase) as shown in Fig. 9.

A DNA sequence which encodes a phytase and which (i) is at least 96.13%; or 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 1-1401 of the DNA sequence of *A. fumigatus* ATCC 13073 alpha-mutant (phytase) shown in Fig. 9. A suitable negative control is DNA encoding *A. fumigatus* 13073 phytase. A suitable positive control is DNA encoding any one of the *A. fumigatus* ATCC 13073 alpha mutant phytase or the optimised alpha-mutant.

(G) Phytases and corresponding DNA sequences related to the optimized *A. fumigatus* alpha-mutant

A phytase that comprises an amino acid sequence that is at least 96.08%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of the phytase of the optimized *A. fumigatus* alpha-mutant.

A phytase that comprises an amino acid sequence that is at least 96.74%; or at least 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of the phytase of the optimized *A. fumigatus* alpha-mutant.

A phytase which is encoded by a DNA sequence which is at least 95.63%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 1-1401 of the DNA sequence encoding the optimized *A. fumigatus* alpha-mutant phytase.

A DNA sequence that encodes a phytase comprising an amino acid sequence that is at least 96.08%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the optimized *A. fumigatus* alpha-mutant phytase.

A DNA sequence which encodes a phytase and which (i) is at least 95.63%; or at least 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, very high stringency conditions to 5 nucleotides 1-1401 of the DNA sequence encoding the optimized *A. fumigatus* alpha-mutant phytase.

A suitable negative control is DNA encoding *A. fumigatus* ATCC 13073 phytase. A suitable positive control is DNA encoding any one of the *A. fumigatus* ATCC 13073 alpha mutant phytase of 10 the optimised alpha-mutant.

(H) Phytases and corresponding DNA sequences related to consensus phytase-7

A phytase that comprises an amino acid sequence which is 15 at least 94.87%; or at least 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-7 as shown in Fig. 10.

A phytase that comprises an amino acid sequence which is at least 95.30%; or at least 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 20 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-7 as shown in Fig. 10.

A phytase which is encoded by a DNA sequence which is at least 96.38%; or 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase- 25 7 shown in Fig. 10.

A DNA sequence which encodes a phytase and which (i) is at least 96.38%; or at least 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical; or (ii) hybridizes under low, or medium, medium/high, high, or very high stringency conditions to nucleotides 12-1412 30 of the DNA sequence of consensus phytase-7 as shown in Fig. 10.

A DNA sequence which encodes a phytase comprising an amino acid sequence which is at least 94.87%; or at least 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-7 as shown in Fig. 10.

(I) Phytases related to basidio consensus phytase

A phytase which comprises an amino acid sequence which is at least 76.23%; or at least 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 94.5, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the combined sequence of (i) amino acids 1-441 of basidio consensus phytase shown in Fig. 3, and (ii) amino acids 1-26 shown in Fig. 5 (the sequence of (ii) to be added at the N-terminus of the sequence of (i)).

A phytase that comprises an amino acid sequence which is at least 79.50%; or at least 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-441 of basidio consensus phytase as shown in Fig. 3.

(J) Phytases related to consensus phytase-12

A phytase which comprises an amino acid sequence which is at least 70, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% identical to the sequence of amino acids 1-467 of consensus phytase-12 as shown in Fig. 21.

A phytase which comprises an amino acid sequence which is at least 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 95.5, 96, 96.5, 97, 97.5, 98, 98.5, 99, 99.5% similar to the sequence of amino acids 1-467 of consensus phytase-12 as shown in Fig. 21.

Table 8

Comparison of phytase amino acid sequences

Phytase	CP10	CP10-thermo (3) - Q50T-K91A	CP1-thermo (8)	CP1-thermo (8) - Q50T-K91A	CP11	CP7	Basidio	A. fumigatus alpha-mutant	A. fumigatus alpha-mutant (opt.)
Consensus phytase-1	95.08/93.79	94.65/93.36	98.50/98.29	98.07/97.86	92.06/90.70	95.29/94.86	69.42/62.16	85.59/82.58	84.73/81.72
A. niger NRRU3135	79.48/76.46	79.05/76.03	80.35/77.75	79.91/77.32	79.27/76.31	84.02/81.64	67.19/59.32	74.07/70.11	74.95/70/99
A. terreus 9-A1	76.04/72.11	75.82/71.90	76.47/72.33	76.25/72.11	76.51/73.02	75.76/71.18	65.39/58.02	69.67/64.84	69.45/64.84
A. terreus cbs	79.04/75.11	78.82/74.89	79.48/75.76	79.26/75.55	77.19/73.27	79.17/75.00	66.92/59.65	72.59/67.76	72.37/67.76
E. nidulans	78.70/74.35	78.26/73.91	79.78/75.87	79.35/75.44	80.56/76.62	76.96/73.04	67.20/58.13	72.39/67.83	72.11/67.54
A. fumigatus 13073	82.93/80.31	82.50/79.87	82.31/79.04	81.88/78.60	81.36/78.64	80.13/76.20	63.54/57.91	97.82/97.16	96.73/96.07
A. fumigatus 32239	81.30/77.39	80.87/76.96	81.09/77.61	80.65/77.17	79.95/76.08	79.13/75.22	63.61/54.97	90.22/86.52	89.57/85.87
T. thermophilus	77.83/73.84	77.38/73.39	78.67/74.89	78.22/74.44	78.47/74.76	76.51/73.15	61.54/54.36	72.01/66.82	72.69/67.49
M. thermophila	69.16/62.81	69.48/63.33	69.27/62.84	69.59/63.36	69.65/63.06	68.82/62.13	65.56/57.91	66.21/58.45	66.44/58.68
T. lanuginosus	73.52/66.70	73.06/66.44	71.92/64.61	71.46/64.16	74.21/68.86	69.50/62.62	67.20/57.41	68.91/61.02	69.61/61.72
P. lycii	64.92/59.10	64.91/59.37	64.46/58.09	64.46/58.36	65.03/59.84	63.13/56.50	77.75/73.07	64.08/57.11	62.47/55.91
A. pediades	64.51/51.81	64.86/51.94	62.98/51.41	63.33/51.54	64.50/52.30	63.05/51.15	78.92/74.71	61.64/52.38	62.13/53.07
P. involutus 1	66.67/58.07	66.67/58.33	64.84/56.51	64.84/56.77	63.30/54.52	65.33/56.53	79.49/76.22	59.59/51.81	59.95/52.20
P. involutus 2	65.54/55.70	65.30/55.53	66.85/56.87	66.58/56.68	66.30/56.35	64.27/54.13	78.09/74.59	61.26/52.62	61.04/52.47

T. pubescens	65.46/57.22	65.72/57.47	62.89/55.67	63.14/55.93	65.03/57.65	63.28/56.51	78.34/75.12	64.08/57.11	62.30/55.24
CP10	-	99.57/99.57	96.57/95.50	96.15/95.08	95.02/94.56	91.01/89.29	70.22/62.28	85.13/82.76	85.99/83.62
CP10t [3] Q50TK91A	99.57/99.57	-	96.15/95.08	96.57/95.50	94.56/94.10	90.58/88.87	70.47/62.28	85.13/82.76	85.99/83.62
CP1thermo [8]	96.57/95.50	96.15/95.08	-	99.57/99.57	93.42/92.29	94.43/93.79	68.40/60.74	84.52/81.94	85.38/82.80
CP1t [8] Q50TK91A	96.15/95.08	96.57/95.50	99.57/99.57	-	92.97/91.84	94.00/93.36	68.64/60.74	84.52/81.94	85.38/82.80
CP1l	95.02/94.56	94.56/94.10	93.42/92.29	92.97/91.84	-	88.44/86.62	68.27/59.73	82.23/79.73	83.37/80.87
CP7	91.01/89.29	90.58/88.87	94.43/93.79	94.00/93.36	88.44/86.62	-	69.80/62.69	81.94/78.71	81.72/78.50
Basidio	70.22/62.28	70.47/62.28	68.40/60.74	68.64/60.74	68.27/59.73	69.80/62.69	-	65.97/60.52	66.41/60.68
A. fumigatus alpha-mut.	85.13/82.76	85.13/82.76	84.52/81.94	84.52/81.94	82.23/79.73	81.94/78.71	65.97/60.52	-	98.93/98.93
A. fum alpha-mut - opt.	85.99/83.62	85.99/83.62	85.38/82.80	85.38/82.80	83.37/80.87	81.72/78.50	66.41/60.68	98.93/98.93	-

Table 9

Comparison of phytase encoding DNA sequences

Phytase	CP10	CP10-thermo[3]-Q50T-K91A	CP1-thermo[8]	CP1-thermo[8]-Q50T-K91A	CP7	Basidio	A. fumigatus alpha-mutant	A. fumigatus alpha-mutant (opt.)
Consensus phytase-1	95.87		98.72	98.36	96.37	65.46	66.88	66.88
A. niger NRRL3135	65.10	64.82	66.10	65.74	67.52	50.68	65.88	66.17
A. terreus 9-A1	61.74	61.53	62.17	62.03	60.53	49.40	66.24	66.31
A. terreus cbs	62.52	62.30	63.02	62.88	61.45	49.74	68.17	68.24
E. nidulans	65.08	64.94	65.30	65.01	64.22	49.92	64.90	65.44
A. fumigatus 13073	65.66	65.38	64.19	64.08	63.65	48.27	96.12	95.62
T. thermophilus	62.52	62.50	62.53	62.66	62.00	52.19	61.77	61.92
M. thermophila	55.51	55.15	55.36	55.22	53.91	48.44	58.17	58.24
T. lanuginosus	57.56	57.20	56.76	56.47	62.00	44.66	59.71	60.07
P. lycii	45.76	46.51	45.14	55.21	55.46	58.50	48.91	49.44
A. pediades	49.89	49.89	49.89	50.11	45.54	61.66	47.49	47.56
P. involutus 1	48.32	49.03	47.81	47.96	49.59	59.80	49.96	50.19
P. involutus 2	48.24	49.00	48.08	48.63	47.94	60.16	47.56	47.63
T. pubescens	47.00	47.17	46.46	47.62	46.83	60.37	49.89	49.96
CP10	-	99.43	96.40	96.05	93.73	66.40	67.81	68.24

CP10t[3]Q50TK91A	99.43	-	96.37	96.58	93.45	66.29	67.81	68.24
Cpithermo[8]	96.40	96.37	-	99.65	95.30	65.40	66.74	67.17
CP1t[8]Q50TK91A	96.05	96.58	99.65	-	94.94	65.47	66.74	67.17
CP7	93.73	93.45	95.30	94.94	-	64.56	65.88	65.88
Basidio	66.40	66.29	65.40	65.47	64.56	-	50.41	50.49
A.fumigatus alpha-mut.	67.81	67.81	66.74	66.74	65.88	50.41	-	99.50
A. fum alpha-mut - opt.	68.24	68.24	67.17	67.17	65.88	50.49	99.50	-

CLAIMS

1. A phytase that comprises an amino acid sequence which is at least 93.80% identical to the sequence of amino acids 1-467 of consensus phytase-10 (SEQ ID NO: 26).

2. A phytase that is encoded by a DNA sequence that is at least 95.88% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 (SEQ ID NO: 25).

3. A phytase that comprises

an amino acid sequence chosen from

(i) SEQ ID NO: 26, or amino acids 1-438 thereof; or

an amino acid sequence encoded by

(ii) nucleotides 12-1412, or 90-1412 of SEQ ID NO: 25.

4. A phytase that comprises

an amino acid sequence chosen from

(i) consensus phytase-10-thermo[3],

(ii) variants of (i), further including the mutations Q50T, K91A, or (Q50T+K91A), the latter variant being shown in Fig. 8,

(iii) amino acids 27-467 of any of the sequences of (i) and (ii),

(iv) SEQ ID NO: 31, or amino acids 1-441 thereof; or

an amino acid sequence encoded by

(v) nucleotides 1-1401, or 79-1401 of SEQ ID NO: 30.

5. A phytase that comprises

an amino acid sequence chosen from

(i) consensus phytase-1-thermo[8],

- (ii) variants of (i), further including the mutations Q50T, K91A, or (Q50T+K91A), the latter variant being shown in Fig. 7,
- (iii) amino acids 27-467 of any of the sequences of (i) and (ii), or
- (iv) SEQ ID NO: 29, or amino acids 1-441 thereof; or an amino acid sequence encoded by
- (v) nucleotides 1-1407, or 79-1407 of SEQ ID NO: 28.

6. A phytase that comprises the amino acid sequence of consensus phytase-11 (SEQ ID NO: 27).

7. A DNA sequence that comprises a DNA-sequence encoding a phytase of any one of claims 1-6.

15

8. A DNA sequence that comprises a DNA-sequence encoding a phytase, and wherein the phytase-encoding DNA-sequence is (i) at least 95.88% identical, or (ii) hybridizes under high stringency conditions, to nucleotides 12-1412 of the DNA sequence of consensus phytase-10 (SEQ ID NO: 25).

9. A DNA sequence that comprises a DNA-sequence that encodes a phytase, wherein the phytase comprises an amino acid sequence that is at least 93.80% identical to the sequence of amino acids 1-467 of consensus phytase 10 (SEQ ID NO: 26).

10. A DNA sequence that comprises a DNA-sequence that encodes a phytase, and wherein the phytase-encoding DNA-sequence comprises

- (i) nucleotides 12-1412, or 90-1412 of the DNA sequence of consensus phytase-10 (SEQ ID NO: 25);

- (ii) nucleotides 1-1401, or 79-1401 of the DNA sequence of consensus phytase-10-thermo[3]-Q50T-K91A (SEQ ID NO: 30); or
- (iii) nucleotides 1-1401, or 79-1401 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T-K91A (SEQ ID NO: 28).

11. A vector comprising a DNA sequence according to any one of claims 7-10.

12. A microbial host cell comprising a DNA sequence according to any one of claims 7-10, or the vector according to claim 11.

13. A process for producing a phytase, the process comprising culturing the host cell according to claim 12 under conditions permitting the production of the phytase, and recovering the phytase from the culture broth.

14. A food, feed or pharmaceutical composition comprising a phytase of any one of claims 1-6.

AMENDED CLAIMS

[received by the International Bureau on 16 June 2000 (16.06.00);
original claims 1 to 14 replaced by new claims 1 to 14 (3 pages)]

1. A phytase that comprises an amino acid sequence which is at least 93.80% identical to the sequence of amino acids -26 to
5 +441 of consensus phytase 10 (SEQ ID NO: 26).

2. A phytase that is encoded by a DNA sequence that is at least 95.88% identical to nucleotides 12-1412 of the DNA sequence of consensus phytase 10 (SEQ ID NO: 25).

10

3. A phytase that comprises
an amino acid sequence chosen from

(i) SEQ ID NO: 26, or amino acids 1-438 thereof; or
an amino acid sequence encoded by

15 (ii) nucleotides 12-1412, or 90-1412 of SEQ ID NO:25.

4. A phytase that comprises
an amino acid sequence chosen from

(i) consensus phytase-10-thermo[3],

20 (ii) variants of (i), further including the mutations
Q50T, K91A, or (Q50T+K91A), the latter variant
being shown in Fig. 8,

(iii) amino acids 27-467 of any of the sequences of (i)
and (ii),

25 (iv) SEQ ID NO: 31, or amino acids 1-441 thereof; or
an amino acid sequence encoded by

(v) nucleotides 1-1401, or 79-1401 of SEQ ID NO:30.

5. A phytase that comprises

30 an amino acid sequence chosen from

(i) consensus phytase-1-thermo[8],

(ii) variants of (i), further including the mutations
Q50T, K91A, or (Q50T+K91A), the latter variant
being shown in Fig. 7,

AMENDED SHEET (ARTICLE 19)

- (iii) amino acids 27-467 of any of the sequences of (i) and (iv), or
- (iv) SEQ ID NO: 29, or amino acids 1-441 thereof; or an amino acid sequence encoded by
- 5 (v) nucleotides 1-1401, or 79-1401 of SEQ ID NO: 28.

6. A phytase that comprises the amino acid sequence of consensus phytase-11 (SEQ ID NO: 27).

10 7. A DNA sequence that comprises a DNA-sequence encoding the phytase of any one of claims 1-6.

8. A DNA sequence that comprises a DNA-sequence encoding a phytase, and wherein the phytase-encoding DNA-sequence is (i) 15 at least 95.88% identical, or (ii) hybridizes under high stringency conditions, to nucleotides 12-1412 of the DNA sequence of consensus phytase 10 (SEQ ID NO: 25).

9. A DNA sequence that comprises a DNA-sequence that encodes a 20 phytase, wherein the phytase comprises an amino acid sequence that is at least 93.80% identical to the sequence of amino acids -26 to + 441 of consensus phytase 10 (SEQ ID NO: 26).

10. A DNA sequence that comprises a DNA-sequence that encodes 25 a phytase, and wherein the phytase-encoding DNA-sequence comprises

- (i) nucleotides 12-1412, or 90-1412 of the DNA sequence of consensus phytase 10 (SEQ ID NO: 25);
- (ii) nucleotides 1-1401, or 79-1401 of the DNA sequence 30 of consensus phytase-10-thermo[3]-Q50T, K91A (SEQ ID NO: 30); or
- (iii) nucleotides 1-1401, or 79-1401 of the DNA sequence of consensus phytase-1-thermo[8]-Q50T, K91A (SEQ ID NO: 28).

11. A vector comprising the DNA sequence according to any one of claims 7-10.

5 12. A microbial host cell comprising the DNA sequence according to any one of claims 7-10, or the vector according to claim 6.

13. A process for producing a phytase, the process comprising
10 culturing the host cell according to claim 12 under conditions permitting the production of the phytase, and recovering the phytase from the culture broth.

14. A food, feed or pharmaceutical composition comprising the
15 phytase of any one of claims 1-6.

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	1		50
<i>A. terreus</i> 9A-1	KhsDCNSVDh	GYQCFPELSH	kwGLYAPYFS LQDESPFP1D VPEDChITFV
<i>A. terreus</i> cbs	NhsDCTSVDr	GYQCFPELSH	kwGLYAPYFS LQDESPFP1D VPDDChITFV
<i>A. niger</i> var. <i>awamori</i>	NqsTCDTVDQ	GYQCFSETSH	LGWQYAPFFS LANESAISPD VPAGCrVTFA
<i>A. niger</i> T213	NqsSCDTVDQ	GYQCFSETSH	LGWQYAPFFS LANESVISPD VPAGCrVTFA
<i>A. niger</i> NRRL3135	NqsSCDTVDQ	GYQCFSETSH	LGWQYAPFFS LANESVISPE VPAGCrVTFA
<i>A. fumigatus</i> 13073	GSKSCDTVD1	GYQCsPATSH	LGWQYSPFFS LEDELsvSSK LPKDCrITLV
<i>A. fumigatus</i> 32722	GSKSCDTVD1	GYQCsPATSH	LGWQYSPFFS LEDELsvSSK LPKDCrITLV
<i>A. fumigatus</i> 58128	GSKSCDTVD1	GYQCsPATSH	LGWQYSPFFS LEDELsvSSK LPKDCrITLV
<i>A. fumigatus</i> 26906	GSKSCDTVD1	GYQCsPATSH	LGWQYSPFFS LEDELsvSSK LPKDCrITLV
<i>A. fumigatus</i> 32239	GSKACDTVE1	GYQCsPGTSH	LGWQYSPFFS LEDELsvSSD LPKDCrVTFV
<i>E. nidulans</i>	QNHSCNTADG	GYQCFPNVSH	VWGQYSPYFS IEQESAISd VPHGCeVTFV
<i>T. thermophilus</i>	DSHSCNTVEG	GYQCrPEISH	swGQYSPFFS LADQSEISPD VPQNCrITFV
<i>M. thermophila</i>	ESRPCDTpD1	GFQCgTAISH	FWGQYSPYFS VpSElDaS.. IPDDCeVTFV
Consensus	NSHSCDTVDG	GYQCFPEISH	LGWQYSPYFS LEDESAISPD VPDDC-VTFV
Consensus phytase	NSHSCDTVDG	GYQCFPEISH	LGWQYSPYFS LEDESAISPD VPDDCrVTFV
	51		100
<i>A. terreus</i> 9A-1	QVLARHGARS	PTThSkKAYA	AtIAAIQKSA TaFpGKYAFL QSYNYSLDSE
<i>A. terreus</i> cbs	QVLARHGARS	PTDSKtKAYA	AtIAAIQKNA TaLpGKYAFL KSYNYSMGSE
<i>A. niger</i> var. <i>awamori</i>	QVLSRHGARY	PTESKgKkYS	ALIEEIQQNV TtFDGKYAFL KTYNYSLGAD
<i>A. niger</i> T213	QVLSRHGARY	PTESKgKkYS	ALIEEIQQNV TtFDGKYAFL KTYNYSLGAD
<i>A. niger</i> NRRL3135	QVLSRHGARY	PTDSKtKkYS	ALIEEIQQNA TtFDGKYAFL KTYNYSLGAD
<i>A. fumigatus</i> 13073	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 32722	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 58128	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 26906	QVLSRHGARY	PTSSKsKkYK	kLVTAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 32239	QVLSRHGARY	PTASKsKkYK	kLVTAIQKNA TeFKGKFAFL ETYNYTLGAD
<i>E. nidulans</i>	QVLSRHGARY	PTESKsKAYS	GLIEAIQKNA TsFwGQYAFL ESYNYTLGAD
<i>T. thermophilus</i>	QLLSRHGARY	PTSSKtELYS	QLISrIQKTA TaYKGyYAFL KDYrYqLGAN
<i>M. thermophila</i>	QVLSRHGARA	PTlKRaasYv	DLIDrIHhGA IsYgPgYEFL RTYDYTLGAD
Consensus	QVLSRHGARY	PTSSK-KAYS	ALIEAIQKNA T-FKGKYAFL KTYNYTLGAD
Consensus phytase	QVLSRHGARY	PTSSKSKAYS	ALIEAIQKNA TAFKGKYAFL KTYNYTLGAD
	101		150
<i>A. terreus</i> 9A-1	ELTPFGrNQL	rDlGaQFYeR	YNALTRhInP FVRATDASRV hESAeKFVEG
<i>A. terreus</i> cbs	NLTPFGrNQL	qDlGaQFYRR	YDTLTRhInP FVRAADSSRV hESAeKFVEG
<i>A. niger</i> var. <i>awamori</i>	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIIP FIRSSGSSRV IASGEKFIEG
<i>A. niger</i> T213	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIIP FIRSSGSSRV IASGEKFIEG
<i>A. niger</i> NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESLTRNIIP FIRSSGSSRV IASGEKFIEG
<i>A. fumigatus</i> 13073	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP FIRASGSDRV IASGEKFIEG
<i>A. fumigatus</i> 32722	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP FIRASGSDRV IASGEKFIEG
<i>A. fumigatus</i> 58128	DLTPFGEQQL	VNSGIKFYQR	YKALARSVVP FIRASGSDRV IASGEKFIEG
<i>A. fumigatus</i> 26906	DLTAFGEQQL	VNSGIKFYQR	YKALARSVVP FIRASGSDRV IASGEKFIEG
<i>A. fumigatus</i> 32239	DLTPFGEQQM	VNSGIKFYQK	YKALAgSVVP FIRSSGSDRV IASGEKFIEG
<i>E. nidulans</i>	DLTiFGENQM	VDSGaKFYRR	YKNLARKnTP FIRASGSDRV VASAeKFING
<i>T. thermophilus</i>	DLTPFGENQM	IQlGIKFYnH	YKSLARNaVP FVRCSGSDRV IASGrIFIEG
<i>M. thermophila</i>	ELTRtGQQQM	VNSGIKFYRR	YRALARKsIP FVRTAGqDRV VhSAENFTQG
Consensus	DLTPFGENQM	VNSGIKFYRR	YKALARK-VP FVRASGSDRV IASAeKFIEG
Consensus phytase	DLTPFGENQM	VNSGIKFYRR	YKALARKIVP FIRASGSDRV IASAeKFIEG

Fig. 1a

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	151		200
<i>A. terreus</i> 9A-1	FQTARqDDHh	ANpHQSPPrV	DVaIPEGsAY NNTLEHs1CT AFES...STV
<i>A. terreus</i> cbs	FQNARqGDPh	ANpHQSPPrV	DVVIPEGtAY NNTLEHs1CT AFEA...STV
<i>A. niger</i> var. <i>awamori</i>	FQSTKLkDPr	AqpgQSSPkI	DVVISeASSs NNTLDPGTCT VFED...SEL
<i>A. niger</i> T213	FQSTKLkDPr	AqpgQSSPkI	DVVISeASSs NNTLDPGTCT VFED...SEL
<i>A. niger</i> NRRL3135	FQSTKLkDPr	AqpgQSSPkI	DVVISeASSs NNTLDPGTCT VFED...SEL
<i>A. fumigatus</i> 13073	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF NNTLDHGVCT kFEA...SQL
<i>A. fumigatus</i> 32722	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF NNTLDHGVCT kFEA...SQL
<i>A. fumigatus</i> 58128	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF NNTLDHGVCT kFEA...SQL
<i>A. fumigatus</i> 26906	FQqAKLADPG	A.TNRAAPAI	SVIIPESETF NNTLDHGVCT kFEA...SQL
<i>A. fumigatus</i> 32239	FQqANVADPG	A.TNRAAPVI	SVIIPESEtY NNTLDHSVCT NFEA...SEL
<i>E. nidulans</i>	FRKAQLhDHG	S..gQATPVV	NVIIPEiDGF NNTLDHSTCV SFEN...DER
<i>T. thermophilus</i>	FQSAKVLDPH	SDkHDAPPTI	NVIIeEGPSY NNTLDtGSCP VFED...SSg
<i>M. thermophila</i>	FHSALLADRG	StvRPTlPyd	mVVIPETAGa NNTLHND1CT AFEEgpySTI
Consensus	FQSAKLADPG	S-PHQASPVI	NVIIPEGSgy NNTLDHGtCT AFED---SEL
Consensus phytase	FQSAKLADPG	SQPHQASPVI	DVIIPEGSgy NNTLDHGtCT AFED...SEL
	201		250
<i>A. terreus</i> 9A-1	GDDAvANFTA	VFAPAIaQRL	EADLPgVqLS TDDVvnlMAM CPFETVS1TD
<i>A. terreus</i> cbs	GDAAADNFTA	VFAPAIakRL	EADLPgVqLS ADDVvnlMAM CPFETVS1TD
<i>A. niger</i> var. <i>awamori</i>	ADTVEANFTA	TFAPSIRQRL	ENDLSGVTLT DTEVtyLMDM CSFDTIstST
<i>A. niger</i> T213	ADTVEANFTA	TFAPSIRQRL	ENDLSGVTLT DTEVtyLMDM CSFDTIstST
<i>A. niger</i> NRRL3135	ADTVEANFTA	TFVPSIRQRL	ENDLSGVTLT DTEVtyLMDM CSFDTIstST
<i>A. fumigatus</i> 13073	GDEVAANFTA	1FAPDIRARa	EkHLPgVTLT DEDVVsLMDM CSFDTVARTS
<i>A. fumigatus</i> 32722	GDEVAANFTA	1FAPDIRARa	EkHLPgVTLT DEDVVsLMDM CSFDTVARTS
<i>A. fumigatus</i> 58128	GDEVAANFTA	1FAPDIRARa	EkHLPgVTLT DEDVVsLMDM CSFDTVARTS
<i>A. fumigatus</i> 26906	GDEVAANFTA	1FAPDIRARa	KkHLPgVTLT DEDVVsLMDM CSFDTVARTS
<i>A. fumigatus</i> 32239	GDEVEANFTA	1FAPAIRARI	EkHLPgVqLT DDDVVsLMDM CSFDTVARTA
<i>E. nidulans</i>	ADEiEANFTA	IMGPPiRkRL	ENDLPgiKLT NENViyLMDM CSFDTMARTA
<i>T. thermophilus</i>	GHDAQEKfak	qFAPAIleKI	KDHLPgVDLa vSDVpyLMDL CPFETLARNh
<i>M. thermophila</i>	GDDAQDTY1S	TFAGPiTarV	NANLPGANLT DADTVaLMDL CPFETVAsSS
Consensus	GDDAEANFTA	TFAPAIRARL	EADLPgVTLT DEDVv-LMDM CPFETVARTS
Consensus phytase	GDDVEANFTA	LFAPAIRARL	EADLPgVTLT DEDVVyLMDM CPFETVARTS
	251		300
<i>A. terreus</i> 9A-1DAhTLSPFC	DLFTAtEWtq YNYLlSLDKY YGYGGGNPLG
<i>A. terreus</i> cbsDAhTLSPFC	DLFTAAEWtq YNYLlSLDKY YGYGGGNPLG
<i>A. niger</i> var. <i>awamori</i>vDTKLSPFC	DLFTHdEWih YDYlQSLkKY YGHGAGNPLG
<i>A. niger</i> T213vDTKLSPFC	DLFTHdEWih YDYlRSLkKY YGHGAGNPLG
<i>A. niger</i> NRRL3135vDTKLSPFC	DLFTHdEWin YDYlQSLkKY YGHGAGNPLG
<i>A. fumigatus</i> 13073DASQLSPFC	QLFTHnEWkk YNYlQSLGKY YGYGAGNPLG
<i>A. fumigatus</i> 32722DASQLSPFC	QLFTHnEWkk YNYlQSLGKY YGYGAGNPLG
<i>A. fumigatus</i> 58128DASQLSPFC	QLFTHnEWkk YNYlQSLGKY YGYGAGNPLG
<i>A. fumigatus</i> 26906DASQLSPFC	QLFTHnEWkk YNYlQSLGKY YGYGAGNPLG
<i>A. fumigatus</i> 32239DASELSPFC	AlFTHnEWkk YDYlQSLGKY YGYGAGNPLG
<i>E. nidulans</i>HGTELSPFC	AlFTEkEWlq YDYlQSLSKY YGYGAGSPLG
<i>T. thermophilus</i>TDT.LSPFC	ALsTQeEWqa YDYYQSLGKY YGnGGGNPLG
<i>M. thermophila</i>	sdpatadagg	gNGrPLSPFC	rLFSEsEWra YDYlQSVGKW YGYGPGNPLG
Consensus	-----	..DATELSPFC	AlFTE-EW-- YDYlQSLGKY YGYGAGNPLG
Consensus phytaseDATELSPFC	AlFTHdEWrq YDYlQSLGKY YGYGAGNPLG

Fig. 1b

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	301			350
<i>A. terreus</i> 9A-1	PVQGVGWaNE	LMARLTRAPV	HDHTCVNNTL	DASPATFPLN ATLYADFSHD
<i>A. terreus</i> cbs	PVQGVGWaNE	LIARLTRSPV	HDHTCVNNTL	DANPATFPLN ATLYADFSHD
<i>A. niger</i> var. <i>awamori</i>	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSNPATFPLN STLYADFSHD
<i>A. niger</i> T213	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSNPATFPLN STLYADFSHD
<i>A. niger</i> NRRL3135	PTQGVGYaNE	LIARLTHSPV	HDDTSSNHTL	DSSPATFPLN STLYADFSHD
<i>A. fumigatus</i> 13073	PAQGIGFtNE	LIARLTRSPV	QDHTSTNStL	vSNPATFPLN ATMYVDFSHD
<i>A. fumigatus</i> 32722	PAQGIGFtNE	LIARLTRSPV	QDHTSTNStL	vSNPATFPLN ATMYVDFSHD
<i>A. fumigatus</i> 58128	PAQGIGFtNE	LIARLTRSPV	QDHTSTNStL	vSNPATFPLN ATMYVDFSHD
<i>A. fumigatus</i> 26906	PAQGIGFtNE	LIARLTRSPV	QDHTSTNStL	vSNPATFPLN ATMYVDFSHD
<i>A. fumigatus</i> 32239	PAQGIGFtNE	LIARLTNSPV	QDHTSTNStL	DSDPATFPLN ATIYVDFSHD
<i>E. nidulans</i>	PAQGIGFtNE	QDNTSTNHTL	DSNPATFPLD	rKLYADFSHD
<i>T. thermophilus</i>	PAQGVGFvNE	LIARMTSPV	QDYTTVNHTL	DSNPATFPLN ATLYADFSHD
<i>M. thermophila</i>	PTQGVGFvNE	LLARLAGvPV	RDgTSTNRTL	DGDPrTFPLG rPLYADFSHD
Consensus	PAQGVGF-NE	LIARLTHSPV	QDHTSTNHTL	DSNPATFPLN ATLYADFSHD
Consensus phytase	PAQGVGFANE	LIARLTRSPV	QDHTSTNHTL	DSNPATFPLN ATLYADFSHD
	351			400
<i>A. terreus</i> 9A-1	SNLVSIFWAL	GLYNGTAPLS	qTSVESVSQT	DGYAAAWTVP FAARAYVEMM
<i>A. terreus</i> cbs	SNLVSIFWAL	GLYNGTkPLS	qTTVEDITrT	DGYAAAWTVP FAARAYIEMM
<i>A. niger</i> var. <i>awamori</i>	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP FASRLYVEMM
<i>A. niger</i> T213	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP FASRLYVEMM
<i>A. niger</i> NRRL3135	NGIISILFAL	GLYNGTkPLS	TTTVENITQT	DGFSSAWTVP FASRLYVEMM
<i>A. fumigatus</i> 13073	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP FGARAYFetM
<i>A. fumigatus</i> 32722	NSMVSIFFAL	GLYNGTGPLS	rTSVESaKEl	DGYSASWVVP FGARAYFetM
<i>A. fumigatus</i> 58128	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP FGARAYFetM
<i>A. fumigatus</i> 26906	NSMVSIFFAL	GLYNGTEPLS	rTSVESaKEl	DGYSASWVVP FGARAYFetM
<i>A. fumigatus</i> 32239	NGMIPiFFAM	GLYNGTEPLS	qTSeESTKES	NGYSASWAVP FGARAYFetM
<i>E. nidulans</i>	NSMISiFFAM	GLYNGTQPLS	mDSVESIQEm	DGYAASWTVP FGARAYFELM
<i>T. thermophilus</i>	NTMTSiFaAL	GLYNGTAKLS	TTEIKSiEET	DGYAAAWTVP FGGRAYIEMM
<i>M. thermophila</i>	NDMMGVLgAL	GaYDGVPLD	KTArrDpEEl	GGYAASWAVP FAARiYVEKM
Consensus	NSMISiFFAL	GLYNGTAPLS	TTSVESIEET	DGYAASWTVP FGARAYVEMM
Consensus phytase	NSMISiFFAL	GLYNGTAPLS	TTSVESIEET	DGYSASWTVP FGARAYVEMM
	401			450
<i>A. terreus</i> 9A-1	QC.....RAEKE	PLVRVLVNDR	VMPLHGCPD KLGRCKrDAF
<i>A. terreus</i> cbs	QC.....RAEQ	PLVRVLVNDR	VMPLHGCAVD NLGRCKrDDF
<i>A. niger</i> var. <i>awamori</i>	QC.....QAEQE	PLVRVLVNDR	VVPLHGCPID aLGRCTrDSF
<i>A. niger</i> T213	QC.....QAEQE	PLVRVLVNDR	VVPLHGCPID aLGRCTrDSF
<i>A. niger</i> NRRL3135	QC.....QAEQE	PLVRVLVNDR	VVPLHGCPVD aLGRCTrDSF
<i>A. fumigatus</i> 13073	QC.....KSEKE	PLVRALINDR	VVPLHGCDVD KLGRCKLNDF
<i>A. fumigatus</i> 32722	QC.....KSEKE	PLVRALINDR	VVPLHGCDVD KLGRCKLNDF
<i>A. fumigatus</i> 58128	QC.....KSEKE	SLVRALINDR	VVPLHGCDVD KLGRCKLNDF
<i>A. fumigatus</i> 26906	QC.....KSEKE	PLVRALINDR	VVPLHGCAVD KLGRCKLNDF
<i>A. fumigatus</i> 32239	QC.....KSEKE	PLVRALINDR	VVPLHGCAVD KLGRCKLNDF
<i>E. nidulans</i>	QC.....E.KKE	PLVRVLVNDR	VVPLHGCAVD KFGRCtLDDW
<i>T. thermophilus</i>	QC.....DDSDE	PVVRVLVNDR	VVPLHGCEVD SLGRCKrDDF
<i>M. thermophila</i>	RCsgggggggg	gggrgQEKE	eMVRVLVNDR	VMtLkGCGAD ERGMCTLErF
Consensus	QC-----	-----QAEKE	PLVRVLVNDR	VVPLHGCAVD KLGRCKLDDF
Consensus phytase	QC.....QAEKE	PLVRVLVNDR	VVPLHGCAVD KLGRCKRDDF

Fig. 1c

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	451	471
<i>A. terreus</i> 9A-1	VAGLSFAQAG	GNWADCF--- ~
<i>A. terreus</i> cbs	VEGLSFARAG	NWAECF---
<i>A. niger</i> var. <i>awamori</i>	VrGLSFARSG	GDWAECsA-- ~
<i>A. niger</i> T213	VrGLSFARSG	GDWAECFA-- ~
<i>A. niger</i> NRRL3135	VrGLSFARSG	DWAECFA--
<i>A. fumigatus</i> 13073	VKGLSWARSG	GNWGECS-- ~
<i>A. fumigatus</i> 32722	VKGLSWARSG	GNWGECS-- ~
<i>A. fumigatus</i> 58128	VKGLSWARSG	GNWGECS-- ~
<i>A. fumigatus</i> 26906	VKGLSWARSG	GNWGECS-- ~
<i>A. fumigatus</i> 32239	VKGLSWARSG	NSEQSFS--
<i>E. nidulans</i>	VEGLNFARSG	GNWkTCFT1~ ~
<i>T. thermophilus</i>	VrGLSFARqG	GNWEGCYAas e
<i>M. thermophila</i>	IESMAFARGN	GKWD1CFA-- ~
Consensus	VEGLSFARSG	GNWAECFA-- -
Consensus phytase	VEGLSFARSG	GNWAECFA.. .

Fig. 1d

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CP-1
 Eco RI M G V F V V L L S I A T L F G S T
 TATATGAATTCATGGGCGTGTTCGTGCTACTGTCCATTGCCACCTTGTTCCGGTTCCA
 1 -----+-----+-----+-----+-----+-----+ 60
 ATATACTTAAGTACCCGACACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGT

S G T A L G P R G N S H S C D T V D G G
 CATCCGGTACCGCCTTGGGTCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTG
 61 -----+-----+-----+-----+-----+-----+ 120
 GTAGGCCATGGCGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACCTGCCAC

CP-2

CP-3
 Y Q C F P E I S H L W G Q Y S P Y F S L
 GTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATACTTCTCTT
 121 -----+-----+-----+-----+-----+-----+ 180
 CAATGGTTACAAAGGGTCTTTAAAGAGTGAACACCCAGTTATGAGAGGTATGAAGAGAA

E D E S A I S P D V P D D C R V T F V Q
 TGGAAGACGAATCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTTCGTTT
 181 -----+-----+-----+-----+-----+-----+ 240
 ACCTTCTGCTTAGACGATAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAG

CP-4

CP-5
 V L S R H G A R Y P T S S K S K A Y S A
 AAGTTTGTCTAGACACGGTGCTAGATACCCAACCTTCTTCTAAGTCTAAGGCTTACTCTG
 241 -----+-----+-----+-----+-----+-----+ 300
 TTCAAAACAGATCTGTGCCACGATCTATGGGTGAAGAAGATTGAGATTCCGAATGAGAC

L I E A I Q K N A T A F K G K Y A F L K
 CTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGA
 301 -----+-----+-----+-----+-----+-----+ 360
 GAAACTAACTTCGATAAGTTTCTTGGATGACGAAAGTTCCCATTCATGCGAAAGAACT

CP-6

CP-7
 T Y N Y T L G A D D L T P F G E N Q M V
 AGACTTACAACCTACACTTTGGGTGCTGACGACTTGACTCCATTTCGGTGAAAACCAAATGG
 361 -----+-----+-----+-----+-----+-----+ 420
 TCTGAATGTTGATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGTTTACC

N S G I K F Y R R Y K A L A R K I V P F
 TTAACCTCTGGTATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCAT
 421 -----+-----+-----+-----+-----+-----+ 480
 AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTA

CP-8

CP-9
 I R A S G S D R V I A S A E K F I E G F
 TCATTAGAGCTTCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTT
 481 -----+-----+-----+-----+-----+-----+ 540
 AGTAATCTCGAAGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACCTTCCAA

Q S A K L A D P G S Q P H Q A S P V I D
 TCCAATCTGCTAAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTG
 541 -----+-----+-----+-----+-----+-----+ 600
 AGGTTAGACGATTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTTCAAGAGGTCAATAAC

Fig. 2a

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CP-10
CP-11
V I I P E G S G Y N N T L D H G T C T A
ACGTTATTATTCCAGAAGGaTCCGGTTACAACAACACTTTGGACCACGGTACTTGTACTG
601 -----+-----+-----+-----+-----+ 660
TGCAATAATAAGGTCTTCCTAGgCCAATGTTGTTGTGAAACCTGGTGCCATGAACATGAC
F E D S E L G D D V E A N F T A L F A P
CTTTCGAAGACTCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTGCTC
661 -----+-----+-----+-----+-----+ 720
GAAAGCTTCTGAGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAG
CP-12
A I R A R L E A D L P G V T L T D E D V
CAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACG
721 -----+-----+-----+-----+-----+ 780
GTCGATAATCTCGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGCTTCTGC
CP-13
V Y L M D M C P F E T V A R T S D A T E
TTGTTTACTTGATGGACATGTGTCCATTGCAAACTGTTGCTAGAACTTCTGACGCTACTG
781 -----+-----+-----+-----+-----+ 840
AACAAATGAACTACCTGTACACAGGTAAGCTTTGACAACGATCTTGAAGACTGCGATGAC
L S P F C A L F T H D E W R Q Y D Y L Q
AATTGCTCTCCATTCTGTGCTTTGTTCACTCACGACGAATGGAGACAATACGACTACTTGC
841 -----+-----+-----+-----+-----+ 900
TTAACAGAGGTAAGACACGAAACAAGTGAGTGCTGCTTACCTCTGTTATGCTGATGAACG
CP-14
CP-15
S L G K Y Y G Y G A G N P L G P A Q G V
AATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTG
901 -----+-----+-----+-----+-----+ 960
TTAGAAACCCATTCTATGATGCCAATGCCACGACCATTGGGTAAACCCAGGTGAGTTCAC
G F A N E L I A R L T R S P V Q D H T S
TTGTTTCGCTAACGAATTGATTGCTAGATTGACTAGATCTCCAGTTCAAGACCACACTT
961 -----+-----+-----+-----+-----+ 1020
AACCAAAGCGATTGCTTAACTAACGATCTAACTGATCTAGAGGTCAAGTTCTGGTGTGAA
CP-16
CP-17
T N H T L D S N P A T F P L N A T L Y A
CTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACG
1021 -----+-----+-----+-----+-----+ 1080
GATGATTGGTGTGAAACCTGAGATTGGGTGATGAAAGGGTAACTTGCGATGAAACATGC
D F S H D N S M I S I F F A L G L Y N G
CTGACTTCTCTCACGACAACCTCTATGATTTCTATTTCTTCGCTTTGGGTTTGTACAACG
1081 -----+-----+-----+-----+-----+ 1140
GACTGAAGAGAGTGCTGTTGAGATACTAAAGATAAAAGAAGCGAAACCCAAACATGTTGC
CP-18
CP-19
T A P L S T T S V E S I E E T D G Y S A
GTACTGCTCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTG
1141 -----+-----+-----+-----+-----+ 1200
CATGACGAGGTAACAGATGATGAAGACAACCTAGATAACTTCTTTGACTGCCAATGAGAC

Fig. 2b

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      S W T V P F G A R A Y V E M M Q C Q A E
CTTCTTGGACTGTTCCATTCCGGTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
1201 -----+-----+-----+-----+-----+-----+ 1260
GAAGAACCTGACAAGGTAAGCCACGATCTCGAATGCAACTTTACTACGTTACAGTTCGAC
                                CP-20
                                CP-21
      K E P L V R V L V N D R V V P L H G C A
AAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
1261 -----+-----+-----+-----+-----+-----+ 1320
TTTTCTTGGTAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

      V D K L G R C K R D D F V E G L S F A R
CTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTGCTA
1321 -----+-----+-----+-----+-----+-----+ 1380
GACAACTGTTCAACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGAT
                                CP-22
      S G G N W A E C F A * Eco RI
GATCTGGTGGTAACTGGGCTGAATGTTTCGCTTAAGAATTCATATA
1381 -----+-----+-----+-----+-----+-----+ 1426
CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT
```

Fig. 2c

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	1				50
<i>P. involutus</i> (phyA1)	SvP.KnTAPt	FPIPeseQrn	WSPYSPYFPL	AeYkAPPAGC	QInQVNIIQR
<i>P. involutus</i> (phyA2)	SvP.RniAPK	FSIPeseQrn	WSPYSPYFPL	AeYkAPPAGC	EInQVNIIQR
<i>T. pubescens</i>	hiPlRdTSAc	LdVTrDvQqs	WSmYSPYFPa	AtYvAPPASC	QInQVHIIQR
<i>A. pediades</i>	GgvvQaTfvQ	pfFPpQiQds	WAAATPYYPV	qaYtPPPkDC	KItQVNIIQR
<i>P. lycii</i>	StQfsfvAAQ	LPiPaQntsn	WGPYdPFFPV	EpYaAPPEGC	tVtQVNLIQR
Basidio	S-P-R-TAAQ	LPiP-Q-Q--	WSPYSPYFPV	A-Y-APPAGC	QI-QVNIIQR
	51				100
<i>P. involutus</i> (phyA1)	HGARFPTSGA	TTRIKAGLTK	LQGVqnfTDA	KFNFIksfky	dLGnsDLVFP
<i>P. involutus</i> (phyA2)	HGARFPTSGA	ATRIKAGLSK	LQSVqnfTDP	KFDFIksfTY	dLGtsDLVFP
<i>T. pubescens</i>	HGARFPTSGA	AkRIQTAVAK	LKAAsnyTDP	lLAFVtNyTY	sLGqDsLVeL
<i>A. pediades</i>	HGARFPTSGA	GTRIQAaVvk	LQSAktyTDP	RLDFLtnyTY	tLGhDDLVPF
<i>P. lycii</i>	HGARWPTSGA	rSRqvAAVAK	IQmArpfTDP	KYEFLnDfvy	kFGvADLLPF
Basidio	HGARFPTSGA	ATRIQAaVAK	LQSA---TDP	KLDfL-N-TY	-LG-DDLVFP
	101				150
<i>P. involutus</i> (phyA1)	GAaQSfDAGQ	EAFARYSkLV	SkNNLPFIRA	dGSDRVVDSA	TNWTAGFAsA
<i>P. involutus</i> (phyA2)	GAaQSfDAGl	EvFARYSkLV	SsDNLPFIRS	dGSDRVVDTA	TNWTAGFAsA
<i>T. pubescens</i>	GAtQSSEAGQ	EAFTRYSSLV	SaDELPFVRA	SGSDRVVATA	nNWTAGFAIA
<i>A. pediades</i>	GAlQSSQAGE	ETfQRYsflV	SkENLPFVRA	SSSNRVVDSA	TNWTegFSaA
<i>P. lycii</i>	GAnQShQTgt	DmYTRYStLf	egGDVPFVRA	AGdQRVVDSS	TNWTAGFGdA
Basidio	GA-QSSQAGQ	EAFTRYs-LV	S-DNLPFVRA	SGSDRVVDSA	TNWTAGFA-A
	151				200
<i>P. involutus</i> (phyA1)	ShNTvqPkLn	LILPQtGNDT	LEDNMCPaAG	DSDPQvNaWL	AVafPSITAR
<i>P. involutus</i> (phyA2)	SrNAiqPkLd	LILPQtGNDT	LEDNMCPaAG	ESDPQvDaWL	AsafPSVTAQ
<i>T. pubescens</i>	SsNSitPvLs	VIISEaGNDT	LDDNMCPaAG	DSDPQvNqWL	AqFAPPMTAR
<i>A. pediades</i>	ShHvlnPiLf	VILSEslNDT	LDDaMCPnAG	sSDPQtGiWt	SIYGTPIAnR
<i>P. lycii</i>	SgETvlPtLq	VVLqEeGNct	LcNNMCPnEv	DGDest.tWL	GVFAPnITAR
Basidio	S-NT--P-L-	VILSE-GNDT	LDDNMCP-AG	DSDPQ-N-WL	AVFAPPITAR
	201				250
<i>P. involutus</i> (phyA1)	LNAAAPSvNL	TDtDAfNLvs	LCAFlTVSke	kkSdFctLFE	giPGsFeAFa
<i>P. involutus</i> (phyA2)	LNAAAPGANL	TDaDAfNLvs	LCPFmTVSke	qkSdFctLFE	giPGsFeAFa
<i>T. pubescens</i>	LNAGAPGANL	TDtDTyNLlt	LCPFETVAtE	rrSeFCDIYE	elQAE.dAFa
<i>A. pediades</i>	LNqqAPGANI	TAAdvsNLip	LCAFETIvKE	tpSpFCNLf.	.tPEEFaqFe
<i>P. lycii</i>	LNAAAPSANL	SDsDAItLmd	MCPFDTLSSG	naSpFCDLf.	.tAEEYvSYe
Basidio	LNAAAPGANL	TD-DA-NL--	LCPFETVS-E	--S-FCDLFE	--PEEF-AF-

Fig. 3a

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	251				300
<i>P. involutus</i> (phyA1)	YgGDLDKfYG	TGYGQeLGPV	QGVGYVNELI	ARLTnsAVRD	NTQTNRTLDA
<i>P. involutus</i> (phyA2)	YaGDLDKfYG	TGYGQALGPV	QGVGYINELL	ARLTnsAVnD	NTQTNRTLDA
<i>T. pubescens</i>	YnADLDKfYG	TGYGQPLGPV	QGVGYINELI	ARLTaQnVsD	HTQTNsTLDS
<i>A. pediades</i>	YfGDLDKfYG	TGYGQPLGPV	QGVGYINELL	ARLTemPVRD	NTQTNRTLDS
<i>P. lycii</i>	YyyDLdKYfYG	TGpGNALGPV	QGVGYVNELL	ARLTgQAVRD	ETQTNRTLDS
Basidio	Y-GDLDKfYG	TGYGQPLGPV	QGVGYINELL	ARLT-QAVRD	NTQTNRTLDS
	301				350
<i>P. involutus</i> (phyA1)	SPvTFPLNKT	FYADFSHDNl	MVAVFSAMGL	FrQPAPLsTS	vPNPwRTWrT
<i>P. involutus</i> (phyA2)	APdTFPLNKT	MYADFSHDNl	MVAVFSAMGL	FrQSAPLsTS	tPDPNRTWLT
<i>T. pubescens</i>	SPeTFPLNRT	LYADFSHDNQ	MVAIFSAMGL	FNQSAPLDPT	tPDPaRTFLv
<i>A. pediades</i>	SPLTFPLDRS	IYADLSHDNQ	MIAIFSAMGL	FNQSSPLDPS	fPNPKRTWVT
<i>P. lycii</i>	dPaTFPLNRT	FYADFSHDNt	MVPIFAALGL	FNaTA.LDPl	kPDENRlWVD
Basidio	SP-TFPLNRT	FYADFSHDNQ	MVAIFSAMGL	FNQSAPLDPS	-PDPNRTWVT
	351				400
<i>P. involutus</i> (phyA1)	SsLVPFSGRM	VVERLsC..f	GT.....tkV	RVLVQDqVQP
<i>P. involutus</i> (phyA2)	SsVVPFSARM	aVERLsC..a	GT.....tkV	RVLVQDqVQP
<i>T. pubescens</i>	kKIVPFSGRM	VVERLdC..g	GA.....qsV	RLLVNDAVQP
<i>A. pediades</i>	SRLtPFSGRM	VtERLlCqrd	GTsgggsri	mrngnvqtfv	RILVNDAVQP
<i>P. lycii</i>	SKLVPFSGHM	tVEKLaC...sgkeaV	RVLVNDAVQP
Basidio	SKLVPFSGRM	VVERL-C---	GT-----	-----V	RVLVNDAVQP
	401				441
<i>P. involutus</i> (phyA1)	LEFCGGDrNG	lCTLakFVES	QtFARsDGaG	DFEKCFATSa	~
<i>P. involutus</i> (phyA2)	LEFCGGDqDG	lCALDkFVES	QaYARsGGaG	DFEKCLATTv	~
<i>T. pubescens</i>	LAFCGADtsG	vCTLDaFVES	QaYARNDGEG	DFEKCFAT--	~
<i>A. pediades</i>	LKFCGGDmDS	lCTLEaFVES	QkYAREdGQG	DFEKCFD---	~
<i>P. lycii</i>	LEFCGG.vDG	vCeLsAFVES	QtYARENGQG	DFAKCgfvPs	e
Basidio	LEFCGGD-DG	-CTLDaFVES	Q-YAREdGQG	DFEKCFATP-	-

Fig. 3b

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	1		50
<i>A. terreus</i> 9a1	KhSDcNSVDh	GYQcFPELSH	kWGLYAPYFS LqDESPPFP1D VPdCHITFV
<i>A. terreus</i> cbs	NhsdCtSVDr	GYQcFPELSH	kWGLYAPYFS LqDESPPFP1D VPdCHITFV
<i>A. niger</i> var. <i>awamori</i>	NqsTCDTVDq	GYQcFSEtSH	LWGQYAPFFS LANESAISPD VPAGCRVTFa
<i>A. niger</i> NRRL3135	NqsSCDTVDq	GYQcFSEtSH	LWGQYAPFFS LANESvISPE VPAGCRVTFa
<i>A. fumigatus</i> 13073	GskSCDTVD1	GYQcSPAtSH	LWGQYSPFFS LEDElSVSSK LPkDCRITLV
<i>A. fumigatus</i> 32722	GskSCDTVD1	GYQcSPAtSH	LWGQYSPFFS LEDElSVSSK LPkDCRITLV
<i>A. fumigatus</i> 58128	GskSCDTVD1	GYQcSPAtSH	LWGQYSPFFS LEDElSVSSK LPkDCRITLV
<i>A. fumigatus</i> 26906	GskSCDTVD1	GYQcSPAtSH	LWGQYSPFFS LEDElSVSSK LPkDCRITLV
<i>A. fumigatus</i> 32239	GskACDTVE1	GYQcSPGtSH	LWGQYSPFFS LEDElSVSSD LPkDCRVTFV
<i>E. nidulans</i>	QNHSCNTaDG	GYQcFPNVSH	VWGQYSPYFS IEQESAISeD VPhGCEvTFV
<i>T. thermophilus</i>	DSHSCNTVEG	GYQCrPEISH	sWGQYSPFFS LADQSEISPD VPqNCKITFV
<i>T. lanuginosus</i>	~~~~~	~~~~~nvDIAR	hWGQYSPFFS LAEvSEISPA VPkGCRVeFV
<i>M. thermophila</i>	ESRPCDTpD1	GFQcGTaISH	FWGQYSPYFS VPSElDaS.. IPdDCEvTFa
Basidio	xSxPxrxTAA	qLPipxQxqx	xWSPYSPYFP VAXyxA.... pPaGcQIXqV
Consensus	NSHSCDTVDG	GYQC-PEISH	LWGQYSPFFS LADESAISPD VP-GCRVTFV
Fcp10	NSHSCDTVDG	GYQCfPEISH	LWGQYSPFFS LADESAISPD VPKGCRVTFV
	51		100
<i>A. terreus</i> 9a1	QVLARHGARS	PThSKTKaYA	AtIaAIQKSA TaFpGKYAFL QSYNYSLDSE
<i>A. terreus</i> cbs	QVLARHGARS	PTdSKTKaYA	AtIaAIQKNA TaLpGKYAFL KSYNYSMGSE
<i>A. niger</i> var. <i>awamori</i>	QVLSRHGARY	PTeSKGKKYS	ALIEEIQQNv TtFDGKYAFL KTYNYSLGAD
<i>A. niger</i> NRRL3135	QVLSRHGARY	PTdSKGKKYS	ALIEEIQQNA TtFDGKYAFL KTYNYSLGAD
<i>A. fumigatus</i> 13073	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 32722	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 58128	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 26906	QVLSRHGARY	PTSSKSKKYk	kLVtAIQaNA TdFKGKFAFL KTYNYTLGAD
<i>A. fumigatus</i> 32239	QVLSRHGARY	PTASKSKKYk	kLVtAIQKNA TeFKGKFAFL ETYNYTLGAD
<i>E. nidulans</i>	QVLSRHGARY	PTeSKSKaYS	GLIEAIQKNA TsFwGQYAFI ESYNYTLGAD
<i>T. thermophilus</i>	QLLSRHGARY	PTSKTELYS	qLIsrIQKtA TaYKGyYAFI KdYrYqLGAN
<i>T. lanuginosus</i>	QVLSRHGARY	PTAhKSEvYA	ELLqrIQDtA TeFKGDFAFL RdYaYhLGAD
<i>M. thermophila</i>	QVLSRHGARA	PTIkRAAsYv	DLIdrIHhGA isYgPgYEFL RTYDYTLGAD
Basidio	NIIQRHGARF	PTSGaAtrIq	AaVakLQsax xxtDPKLDFL xnxTyxLgXd
Consensus	QVLSRHGARY	PTSSKSKKYS	ALI-AIQKNA T-FKGKYAFL KTYNYTLGAD
Fcp10	QVLSRHGARY	PTSSKSKKYS	ALIEAIQKNA TAFKGKYAFL KTYNYTLGAD
	101		150
<i>A. terreus</i> 9a1	ELTPFGrNQL	rDlGaQFYeR	YNAL.TrhIn PFVRATDAsR VhESAekFVE
<i>A. terreus</i> cbs	NLTPFGrNQL	qDlGaQFYRR	YDTL.TrhIn PFVRAADSsR VhESAekFVE
<i>A. niger</i> var. <i>awamori</i>	DLTPFGEQEL	VNSGIKFYQR	YESL.TrnII PFIRSSGSsR VIASGEKFIE
<i>A. niger</i> NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESL.TrnIV PFIRSSGSsR VIASGEKFIE
<i>A. fumigatus</i> 13073	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> 32722	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> 58128	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARsVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> 26906	DLTAFGEQQL	VNSGIKFYQR	YKAL.ARsVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> 32239	DLTPFGEQQM	VNSGIKFYQK	YKAL.AgsVV PFIRSSGSDR VIASGEKFIE
<i>E. nidulans</i>	DLTiFGENQM	VDSGaKfYRR	YKnL.Arknt PFIRASGSDR VVASAEKFIn
<i>T. thermophilus</i>	DLTPFGENQM	IQlGIKFYnH	YKSL.ARnAV PFVRCGSDR VIASGr1FIE
<i>T. lanuginosus</i>	NLTrFGEEQM	MESGrQFYHR	YREq.AReIV PFVRAAGSAR VIASAEfFnr
<i>M. thermophila</i>	ELTRtGQQQM	VNSGIKFYRR	YRAL.ARksI PFVRTAGQDR VVhSAENfCQ
Basidio	DLvPFGAxQs	sQAGqEaFtR	YsxLvSxdnL PFVRASGSDR VVDSAtNWtA
Consensus	DLTPFGEQQM	VNSGIKFYRR	YKAL-AR-IV PFVRASGSDR VIASAEKFIE
Fcp10	DLTPFGEQQM	VNSGIKFYRR	YKAL.ARKIV PFVRASGSDR VIASAEKFIE

Fig. 4a

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	151		200
<i>A. terreus</i> 9a1	GFQTARqDDh	hAnphQPSPr	VDVaIPEGsA YNNTLEHSLC TAFes...St
<i>A. terreus</i> cbs	GFQNARqGDP	hAnphQPSPr	VDVVIPEGtA YNNTLEHSIC TAFEa...St
<i>A. niger</i> var. <i>awamori</i>	GFQSTKLkDP	rAqpgQSSPk	IDVVISEAsS sNNTLDpGtC TvFEd...SE
<i>A. niger</i> NRRL3135	GFQSTKLkDP	rAqpgQSSPk	IDVVISEAsS sNNTLDpGtC TvFEd...SE
<i>A. fumigatus</i> 13073	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT FNNTLDHGVC TkFEa...SQ
<i>A. fumigatus</i> 32722	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT FNNTLDHGVC TkFEa...SQ
<i>A. fumigatus</i> 58128	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT FNNTLDHGVC TkFEa...SQ
<i>A. fumigatus</i> 26906	GFQqAKLADP	gAt.nRAAPa	ISVIIPESeT FNNTLDHGVC TkFEa...SQ
<i>A. fumigatus</i> 32239	GFQqANVADP	gAt.nRAAPV	ISVIIPESeT YNNTLDHSVC TnFEa...SE
<i>E. nidulans</i>	GFRkaQLhDh	g.s.gQATPV	VNVIIPeIdG FNNTLDHStC vSFEn...dE
<i>T. thermophilus</i>	GFQSAKVlDP	hSdKhDAPPt	INVIIeEGpS YNNTLDtGSc PvFEd...Ss
<i>T. lanuginosus</i>	GFQdAKdrDP	rSnkdQAePV	INVIISEEtG sNNTLDgltC PAAEe...Ap
<i>M. thermophila</i>	GFHSALLADR	gStvPTlPy	dmVVIPETaG aNNTLHNDLC TAFEegPySt
Basidio	GFaxA.....	..sxtxxPx	LxVILSExg. .NDTLDDNMCPxAG
Consensus	GFQSAKLADP	-A---QASPV	INVIIPEG-G YNNTLDHGLC TAFE--P-SE
Fcp10	GFQSAKLADP	GANPHQASPV	INVIIPEGAG YNNTLDHGLC TAFE...SE
	201		250
<i>A. terreus</i> 9a1	VGDDAvANFT	AVFAPAIaQR	LEAdLPGVQL StDDVVNLMA MCPFETVSlT
<i>A. terreus</i> cbs	VGDAaADNFT	AVFAPAIaKR	LEAdLPGVQL SADDVVNLMA MCPFETVSlT
<i>A. niger</i> var. <i>awamori</i>	LADtVEANFT	AtFAPSIRqR	LEndLSGVtL TDtEVtyLMD MCSFDtISTs
<i>A. niger</i> NRRL3135	LADtVEANFT	AtFvPSIRqR	LEndLSGVtL TDtEVtyLMD MCSFDtISTs
<i>A. fumigatus</i> 13073	LGDEVAANFT	ALFAPdIRAR	aEkhlPGVtL TDEDVVSIMD MCSFDTVArT
<i>A. fumigatus</i> 32722	LGDEVAANFT	ALFAPdIRAR	aEkhlPGVtL TDEDVVSIMD MCSFDTVArT
<i>A. fumigatus</i> 58128	LGDEVAANFT	ALFAPdIRAR	aEkhlPGVtL TDEDVVSIMD MCSFDTVArT
<i>A. fumigatus</i> 26906	LGDEVAANFT	ALFAPdIRAR	aKkhLPGVtL TDEDVVSIMD MCSFDTVArT
<i>A. fumigatus</i> 32239	LGDEVEANFT	ALFAPAIRAR	IEkhLPGVQL TDDDVVSIMD MCSFDTVArT
<i>E. nidulans</i>	rADEIEANFT	AIMGPPIRkR	LEndLPGIKL TNENViYlMD MCSFDtMArT
<i>T. thermophilus</i>	gGHDAQEKFA	kqFAPILEK	IKDhLPGVDL AvsDVpyLMD LCPFETLArN
<i>T. lanuginosus</i>	.DptqpAEF1	qVFGPRVlKk	ItkhMPGVNL TLEDVplFMD LCPFDTVGsd
<i>M. thermophila</i>	IGDDaQDtYl	StFAGPITaR	VNAnLPGaNL TDADtVaLMD LCPFETVAss
Basidio	dSDpqxnxWl	AVFAPPITaR	LNAAaPGaNL TDxDaxNLxx LCPFETVS..
Consensus	LGDDVEANFT	AVFAPPIRAR	LEA-LPGVNL TDEDVVNLMD MCPFDtVA-T
Fcp10	LGDDVEANFT	AVFAPPIRAR	LEAHLPGVNL TDEDVVNLMD MCPFDTVArT
	251		300
<i>A. terreus</i> 9a1	dD..Aht...LSPF	CDLFtA..tE WtQYNYLlSL dKYYGYGGGN
<i>A. terreus</i> cbs	dD..Aht...LSPF	CDLFtA..aE WtQYNYLlSL dKYYGYGGGN
<i>A. niger</i> var. <i>awamori</i>	Tv..DTK...LSPF	CDLFTH..dE WiHYDYlQSL kKYYGHGAGN
<i>A. niger</i> NRRL3135	Tv..DTK...LSPF	CDLFTH..dE WiNYDYlQSL kKYYGHGAGN
<i>A. fumigatus</i> 13073	SD..ASQ...LSPF	CQLFTH..nE WkKYNyLQSL gKYYGYGAGN
<i>A. fumigatus</i> 32722	SD..ASQ...LSPF	CQLFTH..nE WkKYNyLQSL gKYYGYGAGN
<i>A. fumigatus</i> 58128	SD..ASQ...LSPF	CQLFTH..nE WkKYNyLQSL gKYYGYGAGN
<i>A. fumigatus</i> 26906	SD..ASQ...LSPF	CQLFTH..nE WkKYNyLQSL gKYYGYGAGN
<i>A. fumigatus</i> 32239	AD..ASE...LSPF	CAIFTH..nE WkKYDYlQSL gKYYGYGAGN
<i>E. nidulans</i>	AH..GTE...LSPF	CAIFTE..kE WlQYDYlQSL sKYYGYGAGS
<i>T. thermophilus</i>	ht..DT....LSPF	CALStQ..eE WqaYDYyQSL gKYYGnGGGN
<i>T. lanuginosus</i>	PvlfPrQ...LSPF	CHLFtA..dD WmaYDYyTL dKYYSHGGGS
<i>M. thermophila</i>	SsdpATadag	ggngRpLSPF	CrLFSE..sE WraYDYlQSV gKWYGYGPGN
BasidioxexxSxF	CDLFexxpeE FxaFxYxgdL dKFYGTgYGO
Consensus	SD--ATQ---	-----LSPF	CDLFTH---E W-QYDYlQSL -KYYGYGAGN
Fcp10	SD..ATQ...LSPF	CDLFTH..DE WiQYDYlQSL gKYYGYGAGN

Fig. 4b

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	301		350
<i>A. terreus</i> 9a1	PLGPvQGVGW	aNELMARLTR	A.PVHDHTCv NNTLDASPAT FPLNATLYAD
<i>A. terreus</i> cbs	PLGPvQGVGW	aNELIARLTR	S.PVHDHTCv NNTLDANPAT FPLNATLYAD
<i>A. niger</i> var. <i>awamori</i>	PLGPTQGVGY	aNELIARLTH	S.PVHDDTSS NHTLDSPAT FPLNSTLYAD
<i>A. niger</i> NRRL3135	PLGPTQGVGY	aNELIARLTH	S.PVHDDTSS NHTLDSSPAT FPLNSTLYAD
<i>A. fumigatus</i> 13073	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> 32722	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> 58128	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> 26906	PLGPAQGIGF	tNELIARLTR	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> 32239	PLGPAQGIGF	tNELIARLTN	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>E. nidulans</i>	PLGPAQGIGF	tNELIARLTQ	S.PVQDHTST NsTLvSNPAT FPLNATMYvD
<i>T. thermophilus</i>	PLGPAQGVGF	vNELIARMTg	S.PVQDHTST NHTLDSDPAT FPLNATIYvD
<i>T. lanuginosus</i>	AFGFSRGVGF	vNELIARMTg	NlPVKDHTTt NHTLDdNPET FPLDAvLYAD
<i>M. thermophila</i>	PLGPTQGVGF	vNELLARLA.	GvPVRDgTST NRTLDGDPtT FPLGrPLYAD
Basidio	PLGPvQGVGY	iNELLARLTx	qa.VRDNTqT NRTLDSSPxT FPLNrTFYAD
Consensus	PLGPAQGVGF	-NELIARLTH	S-PVQDHTST NHTLDSPAT FPLNATLYAD
Fcp10	PLGPAQGVGF	VNELIARLTH	S.PVQDHTST NHTLDSPAT FPLNATLYAD
	351		400
<i>A. terreus</i> 9a1	FSHDSnLVSI	FWALGLYNGT	aPLSqtSVE. .SvsQTDGYA AAWTVPFAR
<i>A. terreus</i> cbs	FSHDSnLVSI	FWALGLYNGT	kPLSqtTVE. .ditrTDGYA AAWTVPFAR
<i>A. niger</i> var. <i>awamori</i>	FSHDNGIISI	LFALGLYNGT	kPLSTTVE. .NitQTDGFS SAWTVPFASR
<i>A. niger</i> NRRL3135	FSHDNGIISI	LFALGLYNGT	kPLSTTVE. .NitQTDGFS SAWTVPFASR
<i>A. fumigatus</i> 13073	FSHDNSMVIS	FFALGLYNGT	ePLSrTSVE. .SaKElDGYS ASWvVPFGAR
<i>A. fumigatus</i> 32722	FSHDNSMVIS	FFALGLYNGT	gPLSrTSVE. .SaKElDGYS ASWvVPFGAR
<i>A. fumigatus</i> 58128	FSHDNSMVIS	FFALGLYNGT	ePLSrTSVE. .SaKElDGYS ASWvVPFGAR
<i>A. fumigatus</i> 26906	FSHDNSMVIS	FFALGLYNGT	ePLSrTSVE. .SaKElDGYS ASWvVPFGAR
<i>A. fumigatus</i> 32239	FSHDNGMIPI	FFAMGLYNGT	ePLSqtSeE. .StKESNGYS ASWAVPFAR
<i>E. nidulans</i>	FSHDNSMISI	FFAMGLYNGT	qPLSmdSVE. .SiQEmDGYA ASWTVPFAR
<i>T. thermophilus</i>	FSHDNTMtSI	FaALGLYNGT	akLSTTeIK. .SiEETDGYA AAWTVPFGR
<i>T. lanuginosus</i>	FSHDNTMtGI	FsAMGLYNGT	kPLSTskiQP pTgAAADGYA ASWTVPFAR
<i>M. thermophila</i>	FSHDNDMMGV	LgALGaYDgV	pPLdkTA..R rdpEElGGYA ASWAVPFAR
Basidio	FSHDNQMVAI	FsAMGLFNqS	aPLdPSxpDP nrt....Wv TSklVPFSAR
Consensus	FSHDNTMVIS	FFALGLYNGT	-PLSTTSVEP -S-EETDGYA ASWTVPFAR
Fcp10	FSHDNTMVIS	FFALGLYNGT	KPLSTTSVE. .SIEETDGYA ASWTVPFAR
	401		450
<i>A. terreus</i> 9a1	AYVEMMQC..	ra.....EKEPL VRVLVNDVRM PLHGCPtDKL
<i>A. terreus</i> cbs	AYIEMMQC..	ra.....EKQPL VRVLVNDVRM PLHGCAVDNL
<i>A. niger</i> var. <i>awamori</i>	lyVEMMQC..	Qa.....EQEPL VRVLVNDRVV PLHGCPIDaL
<i>A. niger</i> NRRL3135	lyVEMMQC..	Qa.....EQEPL VRVLVNDRVV PLHGCPVDaL
<i>A. fumigatus</i> 13073	AYfEtMQC..	Ks.....EKEPL VRaLINDRVV PLHGCDVDKL
<i>A. fumigatus</i> 32722	AYfEtMQC..	Ks.....EKEPL VRaLINDRVV PLHGCDVDKL
<i>A. fumigatus</i> 58128	AYfEtMQC..	Ks.....EKESL VRaLINDRVV PLHGCDVDKL
<i>A. fumigatus</i> 26906	AYfEtMQC..	Ks.....EKEPL VRaLINDRVV PLHGCDVDKL
<i>A. fumigatus</i> 32239	AYfEtMQC..	Ks.....EKEPL VRaLINDRVV PLHGCAVDKL
<i>E. nidulans</i>	AYfELMQC..	E.....KKEPL VRVLVNDRVV PLHGCAVDKF
<i>T. thermophilus</i>	AYIEMMQC..	Dd.....sDEPV VRVLVNDRVV PLHGCEVDSL
<i>T. lanuginosus</i>	AYVELLRC..	Etetaseeee	EG...EDEPF VRVLVNDRVV PLHGCrVDRW
<i>M. thermophila</i>	iYVEkMRC..	sggggggggg	EGrqeKDEeM VRVLVNDVRM TLkGCGaDer
Basidio	mvVerLxCxx	xgt:xxxxxxx	xxxxxxxxxxx VRVLVNDaVq PLEfCGGdXd
Consensus	AYVEMMQC--	E-----	EG---EKEPL VRVLVNDRVV PLHGCGVDKL
Fcp10	AYVEMMQC..	EA.....EKEPL VRVLVNDRVV PLHGCGVDKL

Fig. 4c

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	451		482
<i>A. terreus</i> 9a1	GRCKrDAFVA	GLSFAQAG..	GNWADCF--- --
<i>A. terreus</i> cbs	GRCKrDDFVE	GLSFARAG..	GNWAECF--- --
<i>A. niger</i> var. <i>awamori</i>	GRCtrDsFVr	GLSFARSG..	GDWAECsA-- --
<i>A. niger</i> NRRL3135	GRCtrDsFVr	GLSFARSG..	GDWAECFA-- --
<i>A. fumigatus</i> 13073	GRCKlNDFVK	GLSWARSG..	GNWGECFS-- --
<i>A. fumigatus</i> 32722	GRCKlNDFVK	GLSWARSG..	GNWGECFS-- --
<i>A. fumigatus</i> 58128	GRCKlNDFVK	GLSWARSG..	GNWGECFS-- --
<i>A. fumigatus</i> 26906	GRCKlNDFVK	GLSWARSG..	GNWGECFS-- --
<i>A. fumigatus</i> 32239	GRCKlKDFVK	GLSWARSG..	GNSEQSFS-- --
<i>E. nidulans</i>	GRCtlDDWVE	GLNFARSG..	GNWKtCFTl- --
<i>T. thermophilus</i>	GRCKrDDFVr	GLSFARqG..	GNWEGCYAas e-
<i>T. lanuginosus</i>	GRCRrDEWIK	GLTFARqG..	GHWDrCF--- --
<i>M. thermophila</i>	GmCtlErPIE	SMAFARGN..	GKWDlCFA-- --
Basidio	GxCtlDAFVE	SqxYAReDgq	GDFEKCFAtp xx
Consensus	GRCK-DDFVE	GLSFARSG--	GNWEECFA-- --
Fcp10	GRCKRDDFVE	GLSFARSG..	GNWEECFA.. ..

Fig. 4d

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CP-1
 Eco RI M G V F V V L L S I A T L F G S T 17
 TATATGAATTCATGGGCGTGTTCGTGCTACTGTCCATTGCCACCTTGTTTCGGTTCCA
 1 -----+-----+-----+-----+-----+-----+ 60
 ATATACTTAAGTACCCGCACAAGCAGCAGATGACAGGTAACGGTGAACAAGCCAAGGT

 S G T A L G P R G N S H S C D T V D G G 37
 CATCCGGTACCGCCTTGGGTCCTCGTGGTAATTCTCACTCTTGACACTGTTGACGGTG
 61 -----+-----+-----+-----+-----+-----+ 120
 GTAGGCCATGGCGGAACCCAGGAGCACCATTAAAGAGTGAGAACTGTGACAACCTGCCAC
 CP-2
CP-3.10
 Y Q C F P E I S H L W G Q Y S P F F S L 57
 GTTACCAATGTTTCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATTCTTCTCTT
 121 -----+-----+-----+-----+-----+-----+ 180
 CAATGGTTACAAAGGGTCTTTAAAGAGTGAACACCCAGTTATGAGAGGTAAGAAGAGAA

 A D E S A I S P D V P K G C R V T F V Q 77
 TGGCTGACGAATCTGCTATTTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTCGTTCT
 181 -----+-----+-----+-----+-----+-----+ 240
 ACCGACTGCTTAGACGATAAAGAGGTCTGCAAGGTTTCCCGACATCTCAATGAAAGCAAG
CP-4.10
CP-5.10
 V L S R H G A R Y P T S S K S K K Y S A 97
 AAGTTTTGTCTAGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGAAGTACTCTG
 241 -----+-----+-----+-----+-----+-----+ 300
 TTCAAACAGATCTGTGCCACGATCTATGGGTTGAAGAAGATTCAGATTCTTCATGAGAC

 L I E A I Q K N A T A F K G K Y A F L K 117
 CTTTGATTGAAGCTATTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGA
 301 -----+-----+-----+-----+-----+-----+ 360
 GAAACTAAGTTCGATAAGTTTCTTGCATGACGAAAGTTCCCATTCATGCGAAAGAACT
 CP-6
CP-7.10
 T Y N Y T L G A D D L T P F G E Q Q M V 137
 AGACTTACAACCTACACTTTGGGTGCTGACGACTTGACTCCATTCCGGTGAACAACAAATGG
 361 -----+-----+-----+-----+-----+-----+ 420
 TCTGAATGTTGATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTGTTTACC

 N S G I K F Y R R Y K A L A R K I V P F 157
 TTAAGTCTGGTATTAAGTTCTACAGAAGATAACAAGGCTTTGGCTAGAAAGATTGTTCCAT
 421 -----+-----+-----+-----+-----+-----+ 480
 AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTA
CP-8.10
CP-9.10
 V R A S G S D R V I A S A E K F I E G F 177
 TCGTTAGAGCTTCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTTCAATGAAGGTT
 481 -----+-----+-----+-----+-----+-----+ 540
 AGCAATCTCGAAGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAAGTTCCAA

 Q S A K L A D P G A N P H Q A S P V I N 197
 TCCAATCTGCTAAGTTGGCTGACCCAGGTGCTAACCACACCAAGCTTCTCCAGTTATTA
 541 -----+-----+-----+-----+-----+-----+ 600
 AGGTTAGACGATTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAAT

Fig. 5a

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CP-10.10

CP-11.10

V I I P E G A G Y N N T L D H G L C T A 217
 ACGTTATTATTCCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTG
 601 -----+-----+-----+-----+-----+-----+ 660
 TGCAATAATAAGGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGAC

F E E S E L G D D V E A N F T A V F A P 237
 CTTTCGAAGAATCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTCGCTC
 661 -----+-----+-----+-----+-----+-----+ 720
 GAAAGCTTCTTAGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAG

CP-12.10

P I R A R L E A H L P G V N L T D E D V 257
 CACCTATTAGAGCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACG
 721 -----+-----+-----+-----+-----+-----+ 780
 GTGGATAATCTCGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGC

CP-13.10

V N L M D M C P F D T V A R T S D A T Q 277
 TTGTTAACTTGATGGACATGTGTCCATTGACACTGTTGCTAGAACTTCTGACGCTACTC
 781 -----+-----+-----+-----+-----+-----+ 840
 AACAATTGAACTACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAG

L S P F C D L F T H D E W I Q Y D Y L Q 297
 AATTGTCTCCATTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGC
 841 -----+-----+-----+-----+-----+-----+ 900
 TTAACAGAGGTAAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACG

CP-14.10

CP-15.10

S L G K Y Y G Y G A G N P L G P A Q G V 317
 AATCTTTGGGTAAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTG
 901 -----+-----+-----+-----+-----+-----+ 960
 TTAGAAAACCCATTTCATGATGCCAATGCCACGACCATTTGGGTAACCCAGGTCGAGTTCCAC

G F V N E L I A R L T H S P V Q D H T S 337
 TTGGTTTCGTTAACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTT
 961 -----+-----+-----+-----+-----+-----+ 1020
 AACCAGCAATTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAA

CP-16.10

CP-17.10

T N H T L D S N P A T F P L N A T L Y A 357
 CTACTAACCACACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACG
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GATGATTGGTGTGAAACCTGAGATTGGGTCGATGAAAGGGTAACCTTGCGATGAAACATGC

D F S H D N T M V S I F F A L G L Y N G 377
 CTGACTTCTCTCAGACAACACTATGTTTCTATTCTTCTCGCTTTGGGTTTGTACAACG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 GACTGAAGAGAGTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGC

CP-18.10

CP-19.10

T K P L S T T S V E S I E E T D G Y A A 397
 GTACTAAGCCATTGTCTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACGCTG
 1141 -----+-----+-----+-----+-----+-----+ 1200
 CATGATTCCGGTAACAGATGATGAAGACAACCTTAGATAACTTCTTTGACTGCCAATGCGAC

Fig. 5b

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      S W T V P F A A R A Y V E M M Q C E A E 417
      CTTCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTG
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
      GAAGAACCTGACAAGGTAAGCCACGATCTCGAATGCAACTTTACTACGTTACACTTCGAC
                               CP-20.10
                               CP-21.10
      K E P L V R V L V N D R V V P L H G C G 437
      AAAAGGAACCATTTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
      TTTTCCTTGGTAAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC

      V D K L G R C K R D D F V E G L S F A R 457
      GTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTTCGCTA
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
      CACAACCTGTTCAACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGAT
                               CP-22.10
      S G G N W E E C F A * Eco RI 467
      GATCTGGTGGTAACTGGGAAGAATGTTTCGCTTAAGAATTCATATA
1381 -----+-----+-----+-----+-----+-----+-----+ 1426
      CTAGACCACCATTGACCCTTCTTACAAAGCGAATTCTTAAGTATAT

```

Fig. 5c

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	1				50
<i>P. involutus</i> (phyA1)	-----	-FPipeseqR	nWSPYSPYFP	LAeykA....	pPaGCQInqV
<i>P. involutus</i> (phyA2)	-----	-FsipeseqR	nWSPYSPYFP	LAeykA....	pPaGCeInqV
<i>T. pubescens</i>	-----	-LDvtRDVQ	sWSmYSPYFP	aAtyvA....	pPaSCQInqV
<i>A. pediades</i>	-----	-pffpPQIQD	sWAaYTPYFP	VqAyTP....	pPKDCKITqV
<i>P. lycii</i>	-----	-LPipAQnTs	nWGPYdPFFP	VEpyAA....	pPEGCTVTqV
<i>A. terreus</i> 9a1	KhedCNSVDh	GYQcfPELSH	kWGLYAPYFS	LqDESPFP1D	VPEDCHITFV
<i>A. terreus</i> cbs	NhedCtSVDr	GYQcfPELSH	kWGLYAPYFS	LqDESPFP1D	VPDDCHITFV
<i>A. niger</i> var. <i>awamori</i>	NqsTCDTVDq	GYQcfSetSH	LGWQYAPFFS	LANESAISPD	VPaGCRVTFa
<i>A. niger</i> T213	NqsSCDTVDq	GYQcfSetSH	LGWQYAPFFS	LANESvISPD	VPaGCRVTFa
<i>A. niger</i> NRRL3135	NqsSCDTVDq	GYQcfSetSH	LGWQYAPFFS	LANESvISPE	VPaGCRVTFa
<i>A. fumigatus</i> ATCC13073	GSKSCDTVD1	GYQCsPatSH	LGWQYSPFFS	LEDElSVSSK	LPKDCRITLV
<i>A. fumigatus</i> ATCC32722	GSKSCDTVD1	GYQCsPatSH	LGWQYSPFFS	LEDElSVSSK	LPKDCRITLV
<i>A. fumigatus</i> ATCC58128	GSKSCDTVD1	GYQCsPatSH	LGWQYSPFFS	LEDElSVSSK	LPKDCRITLV
<i>A. fumigatus</i> ATCC26906	GSKSCDTVD1	GYQCsPatSH	LGWQYSPFFS	LEDElSVSSK	LPKDCRITLV
<i>A. fumigatus</i> ATCC32239	GSKACDTVEL	GYQCsPGtSH	LGWQYSPFFS	LEDElSVSSD	LPKDCRVTFV
<i>E. nidulans</i>	QNHSCNTaDg	GYQcfPNVSH	VWGQYSPYFS	IEQESAISeD	VPhGCeVTFV
<i>T. thermophilus</i>	DSHSCNTVEG	GYQCrPEISH	sWGQYSPFFS	LADQSEISPD	VPQNCKITFV
<i>T. lanuginosus</i>	-----	-----nvDIAR	hWGQYSPFFS	LAEvSEISPA	VPKGCReVfF
<i>M. thermophila</i>	ESRPCDTpD1	GFQCgTAISH	FWGQYSPYFS	VPsElDaS..	IPDDCeVTFa
Consensus Seq. 11	NSHSCDTVD-	GYQC-PEISH	LGWQYSPFFS	LADESAISPD	VPKGCReVTFV

	51				100
<i>P. involutus</i> (phyA1)	NIIqRHGARF	PTSGaTtRik	AgLtKLQgvq	nftDAKFnFI	KSFKYdLGns
<i>P. involutus</i> (phyA2)	NIIqRHGARF	PTSGaAtRik	AgLsKLQsvq	nftDPKFDFI	KSFYdLGts
<i>T. pubescens</i>	HIIqRHGARF	PTSGaAKRiq	TaVAKLKaaS	nytdP1LAFV	tnYtYSLGqd
<i>A. pediades</i>	NIIqRHGARF	PTSGaGtRiq	AaVKKLQsak	TytdPRLDFL	tnYtYTLGhd
<i>P. lycii</i>	NLIqRHGARW	PTSGarsRqv	AaVAKIQmar	PftDPKYEFL	NdFvYkFGvA
<i>A. terreus</i> 9a1	QVLARHGARS	PThSKTKaYA	AtIAaIQKSA	TaFpGKYAFL	QSYNYSILDSE
<i>A. terreus</i> cbs	QVLARHGARS	PTdSKTKaYA	AtIAaIQKNA	TaLpGKYAFL	KSYNYSMGSE
<i>A. niger</i> var. <i>awamori</i>	QVLSRHGARY	PtESKGGKYS	ALIEeIQQNv	TtFDGKYAFL	KTYNYSLGAD
<i>A. niger</i> T213	QVLSRHGARY	PtESKGGKYS	ALIEeIQQNv	TtFDGKYAFL	KTYNYSLGAD
<i>A. niger</i> NRRL3135	QVLSRHGARY	PTdSKGGKYS	ALIEeIQQNA	TtFDGKYAFL	KTYNYSLGAD
<i>A. fumigatus</i> ATCC13073	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKF AFL	KTYNYTLGAD
<i>A. fumigatus</i> ATCC32722	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKF AFL	KTYNYTLGAD
<i>A. fumigatus</i> ATCC58128	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKF AFL	KTYNYTLGAD
<i>A. fumigatus</i> ATCC26906	QVLSRHGARY	PTSSKSKKYk	kLVtaIQaNA	TdFKGKF AFL	KTYNYTLGAD
<i>A. fumigatus</i> ATCC32239	QVLSRHGARY	PTASKSKKYk	kLVtaIQKNA	TeFKGKF AFL	ETNYNYTLGAD
<i>E. nidulans</i>	QVLSRHGARY	PtESKSKaYS	GLIEaIQKNA	TsFwGQYAFL	ESYNYTLGAD
<i>T. thermophilus</i>	QLLSRHGARY	PTSSKTELYS	qLIsRIQKtA	TaYKGyYAFL	KdYrYqLGAN
<i>T. lanuginosus</i>	QVLSRHGARY	PTAhKSEvYA	ELLQRIQDtA	TeFKGDF AFL	RdYaYhLGAD
<i>M. thermophila</i>	QVLSRHGARA	PTlKRAasYv	DLIDRIHhGA	isYgPgYEFL	RTYDYTLGAD
Consensus Seq. 11	QVLSRHGARY	PTSSKSKKYS	ALIERIQKNA	T-FKGKYAFL	KTYNYTLGAD

Fig. 6a

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	101		150
<i>P. involutus</i> (phyA1)	DLvPFGAaQs	fDAGqEaFaR	YskLvSKNnL PFIRAdGSDR VVDSAtNwTA
<i>P. involutus</i> (phyA2)	DLvPFGAaQs	fDAGLevFaR	YskLvSsDnL PFIRSDGSDR VVDtAtNwTA
<i>T. pubescens</i>	sLveLGAtQs	sEAGqEaFtR	YsSLvSaDeL PFVRASGSDR VVATANNwTA
<i>A. pediades</i>	DLvPFGAlQs	sQAGeEtFQR	YsfLvSKEnL PFVRASSNR VVDSAtNwTE
<i>P. lycii</i>	DLlPFGANQs	hQTGTDMYtR	YsTLfEgGdV PFVRAAGdQR VVDSStNwTA
<i>A. terreus</i> 9a1	ELTPFGrNQL	rDlGaQFYeR	YNAL.TRHIn PFVRATDAsR VhESAeKFVE
<i>A. terreus</i> cbs	NLTPFGrNQL	qDlGaQFYRR	YDTL.TRHIn PFVRAADSsR VhESAeKFVE
<i>A. niger</i> var. <i>awamori</i>	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNII PFIRSSGSsR VIASGEKFIE
<i>A. niger</i> T213	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNII PFIRSSGSsR VIASGEKFIE
<i>A. niger</i> NRRL3135	DLTPFGEQEL	VNSGIKFYQR	YESL.TRNIV PFIRSSGSsR VIASGEKFIE
<i>A. fumigatus</i> ATCC13073	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> ATCC32722	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> ATCC58128	DLTPFGEQQL	VNSGIKFYQR	YKAL.ARSVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> ATCC26906	DLTAfGEQQL	VNSGIKFYQR	YKAL.ARSVV PFIRASGSDR VIASGEKFIE
<i>A. fumigatus</i> ATCC32239	DLTPFGEQQM	VNSGIKFYQK	YKAL.AgSVV PFIRSSGSDR VIASGEKFIE
<i>E. nidulans</i>	DLTiFGENQM	VDSGaKfYRR	YKnL.ARKnT PFIRASGSDR VVASAEKFIN
<i>T. thermophilus</i>	DLTPFGENQM	lQlGIKFYnH	YKSL.ARNvV PFVRCSGSDR VIASGrIFIE
<i>T. lanuginosus</i>	NLTRFGEEQM	MESGrQFYHR	YREq.AREIV PFVRAAGSAR VIASAEfFnr
<i>M. thermophila</i>	ELTRtGQQQM	VNSGIKFYRR	YRAL.ARKSr PFVRTAGQDR VVhSAENfTQ
Consensus Seq. 11	DLTPFGENQM	VNSGIKFYRR	YKAL-ARNIV PFVRASGSDR VIASAEKFIE
	151		200
<i>P. involutus</i> (phyA1)	GFaSA.....	..shNtvqPk	LNLILPQ..T gNDTLEDNMC PAaGD.....
<i>P. involutus</i> (phyA2)	GFaSA.....	..srNaiqPk	LDLILPQ..T gNDTLEDNMC PAaGE.....
<i>T. pubescens</i>	GFaLA.....	..ssNsITPV	LSVIISE..A gNDTLDDNMC PAaGD.....
<i>A. pediades</i>	GFsAA.....	..shHvLNPI	LfVILSE..S LNDTLDDAMC PnaGs.....
<i>P. lycii</i>	GFgdA.....	..sgEtv1Pt	LQVVLQE..E gNcTLcNNMC PnevD.....
<i>A. terreus</i> 9a1	GFQTARqDDh	hAnpHQPSPr	VDVaIPEGSA YNNTLEHSLC TAFES...ST
<i>A. terreus</i> cbs	GFQNARqGDP	hAnpHQPSPr	VDVVIPEGTA YNNTLEHSIC TAFE...ST
<i>A. niger</i> var. <i>awamori</i>	GFQSTKLkDP	rAqpgQSSPk	IDVVISeASS sNNTLDpGtC TvFED...Se
<i>A. niger</i> T213	GFQSTKLkDP	rAqpgQSSPk	IDVVISeASS sNNTLDpGtC TvFED...Se
<i>A. niger</i> NRRL3135	GFQSTKLkDP	rAqpgQSSPk	IDVVISeASS sNNTLDpGtC TvFED...Se
<i>A. fumigatus</i> ATCC13073	GFQqAKLADP	gAt.NRAAPa	ISVIIPeSeT FNNTLDHGVC TkFEA...Sq
<i>A. fumigatus</i> ATCC32722	GFQqAKLADP	gAt.NRAAPa	ISVIIPeSeT FNNTLDHGVC TkFEA...Sq
<i>A. fumigatus</i> ATCC58128	GFQqAKLADP	gAt.NRAAPa	ISVIIPeSeT FNNTLDHGVC TkFEA...Sq
<i>A. fumigatus</i> ATCC26906	GFQqAKLADP	gAt.NRAAPa	ISVIIPeSeT FNNTLDHGVC TkFEA...Sq
<i>A. fumigatus</i> ATCC32239	GFQqANVADP	gAt.NRAAPV	ISVIIPeSeT YNNTLDHSVC TnFEA...Se
<i>E. nidulans</i>	GFRkaQLhDh	g.s.gQATPV	VNVIIPEidG FNNTLDHStC vSFEN...de
<i>T. thermophilus</i>	GFQSAKVlDP	hSdKhDAPpt	INVIIeEGPS YNNTLDtGsC PvFED...SS
<i>T. lanuginosus</i>	GFQdAKdrDP	rSnkDQaEPV	INVIISeETG sNNTLDgltC PAaEE...AP
<i>M. thermophila</i>	GFHSAlLADR	gStvRPTlPy	dmVVIPEtAG aNNTLHNDLC TAFEegpyST
Consensus Seq. 11	GFQSAKLADP	-A--HQASPV	INVIIPEGSG YNNTLDHGLC TAFED---ST

Fig. 6b

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	201		250
<i>P. involutus</i> (phyA1)	.SDpqvnaWl	AVafPSItAR LNAAApsvNL	TDtDafNLVs LCAFItVSK.
<i>P. involutus</i> (phyA2)	.SDpqvDaWl	AsafPSVtAQ LNAAApgANL	TDADafNLVs LCPFmTVSK.
<i>T. pubescens</i>	.SDpqvnQWl	AqFAPPMtAR LNagaPGaNL	TDtDtyNLLt LCPFETVat.
<i>A. pediades</i>	.SDpqtGiWT	SIYGTPianR LNqqaPGaNI	TAADVsnLIp LCAFETIvK.
<i>P. lycii</i>	.GDESt.tWl	GVFAPnItAR LNAAApsaNL	SDsDaLtLMD MCPFDtLSs.
<i>A. terreus</i> 9a1	VGDDAvANFT	AVFAPAIaQR LEAdLPGVQL	StDDVVNLMA MCPFETVSlT
<i>A. terreus</i> cbs	VGDAADNFT	AVFAPAIaKR LEAdLPGVQL	SADDVVNLMA MCPFETVSlT
<i>A. niger</i> var. <i>awamori</i>	LADtveANFT	AtFAPSIRqR LEndLSGVtL	TDtEVtyLMD MCSFDtIStS
<i>A. niger</i> T213	LADtveANFT	AtFAPSIRqR LEndLSGVtL	TDtEVtyLMD MCSFDtIStS
<i>A. niger</i> NRRL3135	LADtveANFT	AtFvPSIRqR LEndLSGVtL	TDtEVtyLMD MCSFDtIStS
<i>A. fumigatus</i> ATCC13073	LGDEvAANFT	ALFAPdIRAR aEkhlPGVtL	TDEDVVSLMD MCSFDtVART
<i>A. fumigatus</i> ATCC32722	LGDEvAANFT	ALFAPdIRAR aEkhlPGVtL	TDEDVVSLMD MCSFDtVART
<i>A. fumigatus</i> ATCC58128	LGDEvAANFT	ALFAPdIRAR aEkhlPGVtL	TDEDVVSLMD MCSFDtVART
<i>A. fumigatus</i> ATCC26906	LGDEvAANFT	ALFAPdIRAR aKkhLPGVtL	TDEDVVSLMD MCSFDtVART
<i>A. fumigatus</i> ATCC32239	LGDEvAANFT	ALFAPdIRAR IEkhLPGVQL	TDDDVVSLMD MCSFDtVART
<i>E. nidulans</i>	rADEiEANFT	AIMGPPIRkR LEndLPGIKL	TNENViYlMD MCSFDtMART
<i>T. thermophilus</i>	gGHDAQEKFA	kqFAPAILEK IKDhLPGVDL	AvsDVpyLMD LCPFETLArn
<i>T. lanuginosus</i>	.DptqpAEFl	qVFGPRVlkK ItkhMPGVNL	TLEDVplFMD LCPFDtVGsd
<i>M. thermophila</i>	IGDDAQDtYl	StFAGPiTar VNanLPgaNL	TDADtValMD LCPFETVAss
Consensus Seq. 11	LGDDAEANFT	AVFAPPiRAR	LEA-LPGVNL
		TDEDVVNLMD	MCPFDtVART
	251		300
<i>P. involutus</i> (phyA1)ekkSdF	CtLFegiPGs FeaFAYggdL dKfYgtGyGQ
<i>P. involutus</i> (phyA2)eqkSdF	CtLFegiPGs FeaFAYagdL dKfYgtGyGQ
<i>T. pubescens</i>errSeF	CDIYeelqAE .daFAYnadL dKfYgtGyGQ
<i>A. pediades</i>etpSPF	CNLF..TPEE FaQFEYFgdL dKfYgtGyGQ
<i>P. lycii</i>gnaSPF	CDLF..TAAE YvsYEYYdL dKYYgtGPGN
<i>A. terreus</i> 9a1	dD..Aht...LSPF	CDLF..TAtE WtQYNYLlSL dKYYGYGGGN
<i>A. terreus</i> cbs	dD..Aht...LSPF	CDLF..TAAE WtQYNYLlSL dKYYGYGGGN
<i>A. niger</i> var. <i>awamori</i>	Tv..DTK...LSPF	CDLF..ThDE WiHYDYLQSL kKYYGHGAGN
<i>A. niger</i> T213	Tv..DTK...LSPF	CDLF..ThDE WiHYDYLRLSL kKYYGHGAGN
<i>A. niger</i> NRRL3135	Tv..DTK...LSPF	CDLF..ThDE WiNYDYQLQSL kKYYGHGAGN
<i>A. fumigatus</i> ATCC13073	SD..ASQ...LSPF	CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
<i>A. fumigatus</i> ATCC32722	SD..ASQ...LSPF	CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
<i>A. fumigatus</i> ATCC58128	SD..ASQ...LSPF	CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
<i>A. fumigatus</i> ATCC26906	SD..ASQ...LSPF	CQLF..ThNE WkKYNYLQSL gKYYGYGAGN
<i>A. fumigatus</i> ATCC32239	AD..ASE...LSPF	CAIF..ThNE WkKYDYQLQSL gKYYGYGAGN
<i>E. nidulans</i>	AH..GTE...LSPF	CAIF..TEKE WlQYDYQLQSL sKYYGYGAGS
<i>T. thermophilus</i>	ht..DT....LSPF	CALs..TqEE WqaYDYyQSL gKYYGnGGGN
<i>T. lanuginosus</i>	PvlfPrQ...LSPF	CHLF..TADD WmaYDYyTL dKYYSHGGGS
<i>M. thermophila</i>	SsdpaTadag	ggngRPLSPF	CrLF..SEsE WrayDYQLQSV gKWYGYGPGN
Consensus Seq. 11	SD--ATQ---	-----LSPF	CDLF--TADE
			W-QYDYQLQSL -KYYGYGAGN

Fig. 6c

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	301		350
<i>P. involutus</i> (phyA1)	eLGPvQGVGY vNELIARLTN	S.AVRDNTqT	NRTLDA SPvT FPLNkTFYAD
<i>P. involutus</i> (phyA2)	ALGPvQGVGY iNELLARLTN	S.AVNDNTqT	NRTLDAaPDT FPLNkTMAYAD
<i>T. pubescens</i>	PLGPvQGVGY iNELIARLTa	q.nVsDHTqT	NsTLDS SPET FPLNrTLAYAD
<i>A. pediades</i>	PLGPvQGVGY iNELLARLTE	m.PVRDNTqT	NRTLDS SPIT FPLDrSIYAD
<i>P. lycii</i>	ALGPvQGVGY vNELLARLTg	q.AVRDETqT	NRTLDS DPAT FPLNrTFYAD
<i>A. terreus</i> 9a1	PLGPvQGVGW aNELMARLTR	A.PVHDHTCv	NNTLDA SPAT FPLNATLYAD
<i>A. terreus</i> cbs	PLGPvQGVGW aNELIARLTR	S.PVHDHTCv	NNTLDA NPAT FPLNATLYAD
<i>A. niger</i> var. <i>awamori</i>	PLGPTQGVGY aNELIARLTH	S.PVHDDTSS	NHTLDS NPAT FPLNSTLYAD
<i>A. niger</i> T213	PLGPTQGVGY aNELIARLTH	S.PVHDDTSS	NHTLDS NPAT FPLNSTLYAD
<i>A. niger</i> NRRL3135	PLGPTQGVGY aNELIARLTH	S.PVHDDTSS	NHTLDS SPAT FPLNSTLYAD
<i>A. fumigatus</i> ATCC13073	PLGPAQGIGF tNELIARLTR	S.PVQDHTST	NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> ATCC32722	PLGPAQGIGF tNELIARLTR	S.PVQDHTST	NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> ATCC58128	PLGPAQGIGF tNELIARLTR	S.PVQDHTST	NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> ATCC26906	PLGPAQGIGF tNELIARLTR	S.PVQDHTST	NsTLvSNPAT FPLNATMYvD
<i>A. fumigatus</i> ATCC32239	PLGPAQGIGF tNELIARLTN	S.PVQDHTST	NsTLDS DPAT FPLNATIYvD
<i>E. nidulans</i>	PLGPAQGIGF tNELIARLTQ	S.PVQDNTST	NHTLDS NPAT FPLDrkLYAD
<i>T. thermophilus</i>	PLGPAQGVGF vNELIARMTg	S.PVQDYTTv	NHTLDS NPAT FPLNATLYAD
<i>T. lanuginosus</i>	AFGPSRGVGF vNELIARMTg	NlPVKDHTTv	NHTLDdNPET FPLDAvLYAD
<i>M. thermophila</i>	PLGPTQGVGF vNELLARLA	GvPVRDgTST	NRTLGDPrT FPLGrPLYAD
Consensus Seq. 11	PLGPAQGVGF -NELIARLTH	S-PVQDHTST	NHTLDS NPAT FPLNATLYAD
	351		400
<i>P. involutus</i> (phyA1)	FSHDNlMVAV FsAMGLFrqP	aPLSTSVpNP	wrt.....Wr TSSLVPFSGR
<i>P. involutus</i> (phyA2)	FSHDNlMVAV FsAMGLFrqS	aPLSTSTpDP	nrt.....Wl TSSvVPFSAR
<i>T. pubescens</i>	FSHDNqMVAI FsAMGLFNqS	aPLdPTTpDP	art.....Fl vkkiVPFSAR
<i>A. pediades</i>	LSHDNqMIAI FsAMGLFNqS	sPLdPSfpNP	krt.....Wv TSRLtPFSAR
<i>P. lycii</i>	FSHDNTMVPI FaALGLFNAT	a.LdPlkpDe	nrl.....Wv DSKlVPFSGH
<i>A. terreus</i> 9a1	FSHDSnLVSI FWALGLYNGT	aPLSqtSVES	Vs..QTDGYA AAWTVPFAAR
<i>A. terreus</i> cbs	FSHDSnLVSI FWALGLYNGT	KPLSqtTVEd	It..rTDGYA AAWTVPFAAR
<i>A. niger</i> var. <i>awamori</i>	FSHDNGIISI LFALGLYNGT	KPLSTTTVEN	It..QTDGFS SAWTVPFASR
<i>A. niger</i> T213	FSHDNGIISI LFALGLYNGT	KPLSTTTVEN	It..QTDGFS SAWTVPFASR
<i>A. niger</i> NRRL3135	FSHDNGIISI LFALGLYNGT	KPLSTTTVEN	It..QTDGFS SAWTVPFASR
<i>A. fumigatus</i> ATCC13073	FSHDNSMVISI FFALGLYNGT	EPLSrTSVES	ak..ElDGYS ASWvVPFGAR
<i>A. fumigatus</i> ATCC32722	FSHDNSMVISI FFALGLYNGT	gPLSrTSVES	ak..ElDGYS ASWvVPFGAR
<i>A. fumigatus</i> ATCC58128	FSHDNSMVISI FFALGLYNGT	EPLSrTSVES	ak..ElDGYS ASWvVPFGAR
<i>A. fumigatus</i> ATCC26906	FSHDNSMVISI FFALGLYNGT	EPLSrTSVES	ak..ElDGYS ASWvVPFGAR
<i>A. fumigatus</i> ATCC32239	FSHDNGMIPI FFAMGLYNGT	EPLSqtSeES	tk..ESNGYS ASWAVPFGAR
<i>E. nidulans</i>	FSHDNSMISI FFAMGLYNGT	QPLSmdSVES	Iq..EmDGYA ASWTVPFGAR
<i>T. thermophilus</i>	FSHDNTMtSI FaALGLYNGT	akLSTTeIKS	Ie..ETDGYS AAWTVPFGGR
<i>T. lanuginosus</i>	FSHDNTMtGI FsAMGLYNGT	KPLSTSkIQP	ptgaAADGYA ASWTVPFAAR
<i>M. thermophila</i>	FSHDNMMGV LgALGaYDgV	pPLdkTArrd	..peElGGYA ASWAVPFAAR
Consensus Seq. 11	FSHDNTMVISI FFALGLYNGT	KPLSTTSVES	I---ETDGYS ASWTVPFAAR

Fig. 6d

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	401		450
<i>P. involutus</i> (phyA1)	mvVErLsC.. fGt..... Tk	VRVLVQDQVq	PLEfCGgDRn
<i>P. involutus</i> (phyA2)	maVErLsC.. AGt..... Tk	VRVLVQDQVq	PLEfCGgDQd
<i>T. pubescens</i>	mvVErLDC.. GGa..... Qs	VRLLVNDaVq	PLafCGaDts
<i>A. pediades</i>	mvtErLlCQr DGtGsGGpsr	imrNgnvQTF	VRILVNDaLq
<i>P. lycii</i>	mtVEkLaC..sgKea	VRVLVNDaVq	PLEfCGg.vd
<i>A. terreus</i> 9a1	AYVEMMQCrAEK...EPL	VRVLVNDRVM
<i>A. terreus</i> cbs	AYIEMMQCrAEK...QPL	VRVLVNDRVM
<i>A. niger</i> var. <i>awamori</i>	lYVEMMQCQAEQ...EPL	VRVLVNDRVV
<i>A. niger</i> T213	lYVEMMQCQAEQ...EPL	VRVLVNDRVV
<i>A. niger</i> NRRL3135	lYVEMMQCQAEQ...EPL	VRVLVNDRVV
<i>A. fumigatus</i> ATCC13073	AYfEtMQCKsEK...EPL	VraLINDRVV
<i>A. fumigatus</i> ATCC32722	AYfEtMQCKsEK...EPL	VraLINDRVV
<i>A. fumigatus</i> ATCC58128	AYfEtMQCKsEK...ESL	VraLINDRVV
<i>A. fumigatus</i> ATCC26906	AYfEtMQCKsEK...EPL	VraLINDRVV
<i>A. fumigatus</i> ATCC32239	AYfEtMQCKsEK...EPL	VraLINDRVV
<i>E. nidulans</i>	AYfELMQCE.KK...EPL	VRVLVNDRVV
<i>T. thermophilus</i>	AYIEMMQCDDsD...EPV	VRVLVNDRVV
<i>T. lanuginosus</i>	AYVELLRCEt ETsSeEEeEG	..ED...EPF	VRVLVNDRVV
<i>M. thermophila</i>	iYVEkMRCSG GGgGgGGgEG	..rQekdEeM	VRVLVNDRVM
Consensus Seq. 11	AYVEMMQCEA GG-G-GG-EG	--EK---EPL	VRVLVNDRVV
	451		482
<i>P. involutus</i> (phyA1)	GlCtLAKFVE SqTFARSDga	GDFEKCFAts	a~
<i>P. involutus</i> (phyA2)	GlCaLDKFVE SqAYARSGga	GDFEKCLAtt	v~
<i>T. pubescens</i>	GvCtLDAFVE SqAYARNDge	GDFEKCFAt~	--
<i>A. pediades</i>	SlCtLEAFVE SqkYAReDgq	GDFEKCFD~	--
<i>P. lycii</i>	GvCElSAFVE SqTYAReNgq	GDFAKCgfv	se
<i>A. terreus</i> 9a1	GRCKrDAFVA GLSFAQAG..	GNWADCF---	--
<i>A. terreus</i> cbs	GRCKrDDFVE GLSFARAG..	GNWAECF---	--
<i>A. niger</i> var. <i>awamori</i>	GRCtrDsFVr GLSFARSG..	GDWAECsA--	--
<i>A. niger</i> T213	GRCtrDsFVr GLSFARSG..	GDWAECFA--	--
<i>A. niger</i> NRRL3135	GRCtrDsFVr GLSFARSG..	GDWAECFA--	--
<i>A. fumigatus</i> ATCC13073	GRCKLNDFVK GLSWARSG..	GNWGECSF--	--
<i>A. fumigatus</i> ATCC32722	GRCKLNDFVK GLSWARSG..	GNWGECSF--	--
<i>A. fumigatus</i> ATCC58128	GRCKLNDFVK GLSWARSG..	GNWGECSF--	--
<i>A. fumigatus</i> ATCC26906	GRCKLNDFVK GLSWARSG..	GNWGECSF--	--
<i>A. fumigatus</i> ATCC32239	GRCKLKDFVK GLSWARSG..	GNSEQSFS--	--
<i>E. nidulans</i>	GRCTLDDWVE GLNFARSG..	GNWktCFTl~	--
<i>T. thermophilus</i>	GRCKrDDFVr GLSFARqG..	GNWEGCYAas	e-
<i>T. lanuginosus</i>	GRCRrDEWIK GLTFARqG..	GHWDrCF---	--
<i>M. thermophila</i>	GmCtLErFIE SMAFARGN..	GKWDlCFA--	--
Consensus Seq. 11	GRCKLDDFVE GLSFARSG--	GNWAECFA--	--

Fig. 6e

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M G V F V V L L S I A T L F G S T S G T      20
ATGGGCGTGTTTCGTGCTACTGTCCATTGCCACCTTGTTTCGGTTCACATCCGGTACC
1  -----+-----+-----+-----+-----+-----+-----+
TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG      60

A L G P R G N S H S C D T V D G G Y Q C      40
GCCTTGGGTCCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61 -----+-----+-----+-----+-----+-----+-----+
CGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACCTGCCACCAATGGTTACA      120

F P E I S H L W G T Y S P Y F S L A D E      60
TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
121 -----+-----+-----+-----+-----+-----+-----+
AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT      180

S A I S P D V P D D C R V T F V Q V L S      80
TCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTTCGTTCAAGTTTGTCT
187 -----+-----+-----+-----+-----+-----+-----+
AGACGATAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAGTTCAAAACAGA      240

R H G A R Y P T S S A S K A Y S A L I E      100
AGACACGGTGCTAGATACCCAACCTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+-----+
TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAACTT      300

A I Q K N A T A F K G K Y A F L K T Y N      120
GCTATTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301 -----+-----+-----+-----+-----+-----+-----+
CGATAAGTTTTCTTGCATGACGAAAGTTCCCATTTCATGCGAAAGAACTTCTGAATGTTG      360

Y T L G A D D L T P F G E N Q M V N S G      140
TACACTTTGGGTGCTGACGACTTGACTCCATTTCGGTGAAAACCAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+-----+
ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACCAATTGAGACCA      420

I K F Y R R Y K A L A R K I V P F I R A      160
ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTTCATTAGAGCT
421 -----+-----+-----+-----+-----+-----+-----+
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA      480

S G S D R V I A S A E K F I E G F Q S A      180
TCTGGTTCCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+-----+
AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACCTCCAAAGGTTAGACGA      540

K L A D P G S Q P H Q A S P V I N V I I      200
AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
541 -----+-----+-----+-----+-----+-----+-----+
TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTTGAAGAGGTCAATAATTGCACTAGTAA      600

P E G S G Y N N T L D H G T C T A F E D      220
CCAGAAGGATCCGTTACAACAACACTTTGGACCACGGTACTTGTACTGCTTTTGAAGAC
601 -----+-----+-----+-----+-----+-----+-----+
GGTCTTCCTAGGCCAATGTTGTTGTGAAACCTGGTGCCATGAACATGACGAAAGCTTCTG      660

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Fig. 7a

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S E L G D D V E A N F T A L F A P A I R 240
TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTTCGCTCCAGCTATTAGA
661 -----+-----+-----+-----+-----+-----+ 720
AGACTTAATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTCGATAATCT

A R L E A D L P G V T L T D E D V V Y L 260
GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG
721 -----+-----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGACTGAACGGTCCACAATGAACTGACTGCTTCTGCAACAAATGAAC

M D M C P F D T V A R T S D A T E L S P 280
ATGGACATGTGTCCATTGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
781 -----+-----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAGCGATCTTGAAGACTGCGATGACTTAACAGAGGT

F C A L F T H D E W I Q Y D Y L Q S L G 300
TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
841 -----+-----+-----+-----+-----+-----+ 900
AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTTCGAACCCA

K Y Y G Y G A G N P L G P A Q G V G F A 320
AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT
901 -----+-----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTGGGTAAACCCAGGTCGAGTTCACAACCAAAGCGA

N E L I A R L T H S P V Q D H T S T N H 340
AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+-----+ 1020
TTGCTTAACCTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

T L D S N P A T F P L N A T L Y A D F S 360
ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

H D N T M I S I F F A L G L Y N G T K P 380
CACGACAACACTATGATATCTATTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081 -----+-----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCCGT

L S T T S V E S I E E T D G Y S A S W T 400
TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGACT
1141 -----+-----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

V P F A A R A Y V E M M Q C Q A E K E P 420
GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

L V R V L V N D R V V P L H G C A V D K 440
TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+-----+ 1320
AACCAATCTCAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACCTGTTTC

Fig. 7b

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      L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G      460
      TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+ 1380
      AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

      N  W  A  E  C  F  A  *      467
      AACTGGGCTGAATGTTTCGCTTAA
1381 -----+-----+----- 1410
      TTGACCCGACTTACAAAGCGAATT
```

Fig. 7c

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M G V F V V L L S I A T L F G S T S G T      20
ATGGGCGTGTTCGTTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCACATCCGGTACC
1 -----+-----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCAGCATGACAGGTAACGGTGAACAAGCCAAGGTGTAGGCCATGG

A L G P R G N S H S C D T V D G G Y Q C      40
GCCTTGGGTCCCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61 -----+-----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTGAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

F P E I S H L W G T Y S P F F S L A D E      60
TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA
121 -----+-----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTTAAAGAGTGAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

S A I S P D V P K G C R V T F V Q V L S      80
TCTGCTATTTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTTCGTTCAAGTTTTGTCT
181 -----+-----+-----+-----+-----+-----+-----+ 240
AGACGATAAAGAGGTCTGCAAGGTTTCCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

R H G A R Y P T S S A S K A Y S A L I E      100
AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCGTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGCATGAGACGAACTAACTT

A I Q K N A T A F K G K Y A F L K T Y N      120
GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301 -----+-----+-----+-----+-----+-----+-----+ 360
CGATAAGTTTTCTTGCATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

Y T L G A D D L T P F G E Q Q M V N S G      140
TACACTTTGGGTGCTGACGACTTGACTCCATTCCGGTGAACAACAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTTGTTTACCAATTGAGACCA

I K F Y R R Y K A L A R K I V P F I R A      160
ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCTTAGAGCT
421 -----+-----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

S G S D R V I A S A E K F I E G F Q S A      180
TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

K L A D P G A N P H Q A S P V I N V I I      200
AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
541 -----+-----+-----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCACGATTGGGTGTGGTTCGAAGAGGTCAATAATTGCAATAATAA

P E G A G Y N N T L D H G L C T A F E E      220
CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA
601 -----+-----+-----+-----+-----+-----+-----+ 660
GGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

```

Fig. 8a

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```

S E L G D D V E A N F T A V F A P P I R      240
TCTGAATTGGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA
661 -----+-----+-----+-----+-----+-----+-----+ 720
AGACTTAACCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

A R L E A H L P G V N L T D E D V V N L      260
GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG
721 -----+-----+-----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

M D M C P F D T V A R T S D A T Q L S P      280
ATGGACATGTGTCCATTTCGACACTGTTGCTAGAACCTTCTGACGCTACTCAATTGTCTCCA
781 -----+-----+-----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

F C D L F T H D E W I Q Y D Y L Q S L G      300
TTCTGTGACTTGTTCACCTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
841 -----+-----+-----+-----+-----+-----+-----+ 900
AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

K Y Y G Y G A G N P L G P A Q G V G F V      320
AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
901 -----+-----+-----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTGGGTAACCCAGGTGAGTTCACACAACCAAAGCAA

N E L I A R L T H S P V Q D H T S T N H      340
AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TTGCTTAACCTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

T L D S N P A T F P L N A T L Y A D F S      360
ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGCGATGAAAGGGTAACCTTGCATGAAACATGCGACTGAAGAGA

H D N T M V S I F F A L G L Y N G T K P      380
CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCCGGT

L S T T S V E S I E E T D G Y S A S W T      400
TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

V P F A A R A Y V E M M Q C E A E K E P      420
GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCCTTGGT

L V R V L V N D R V V P L H G C G V D K      440
TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGGTGTGACAAG
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACCACAACCTGTT

```

Fig. 8b

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```
      L  G  R  C  K  R  D  D  F  V  E  G  L  S  F  A  R  S  G  G      460
      TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+ 1380
      AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

      N  W  E  E  C  F  A  *      467
      AACTGGGAAGAATGTTTCGCTTAA
1381 -----+-----+----- 1404
      TTGACCCTTCTTACAAAGCGAATT
```

Fig. 8c

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M G V F V V L L S I A T L F G S T S G T 20
ATGGGGGTTTTCGTCGTTCTATTATCTATCGCGACTCTGTTCGGCAGCACATCGGGCACT
1 -----+-----+-----+-----+-----+ 60
TACCCCCAAAAGCAGCAAGATAATAGATAGCGCTGAGACAAGCCGTCGTGTAGCCCGTGA

A L G P R G N H S K S C D T V D L G Y Q 40
GCGCTGGGCCCCCGTGGAATCACTCCAAGTCCTGCGATACGGTAGACCTAGGGTACCAG
61 -----+-----+-----+-----+-----+ 120
CGCGACCCGGGGGCACCTTTAGTGAGGTTTCAAGACGCTATGCCATCTGGATCCCATGGTC

C S P A T S H L W G T Y S P Y F S L E D 60
TGCTCCCTGCGACTTCTCATCTATGGGGCAGTACTCGCCATaCTTTTCGCTCGAGGAC
121 -----+-----+-----+-----+-----+ 180
ACGAGGGGACGCTGAAGAGTAGATAACCCGtgCATGAGCGGTatGAAAAGCGAGCTCCTG

E L S V S S K L P K D C R I T L V Q V L 80
GAGCTGTCCGTGTCGAGTAAGCTTCCCAAGGATTGCCGGATCACCTTGGTACAGGTGCTA
181 -----+-----+-----+-----+-----+ 240
CTCGACAGGCACAGCTCATTCGAAGGGTTCCTAACGGCCTAGTGGAACCATGTCCACGAT

S R H G A R Y P T S S K S K K Y K K L I 100
TCGCGCCATGGAGCGCGGTACCCAACCAGCTCCAAGAGCAAAAAGTATAAGAAGCTTaTt
241 -----+-----+-----+-----+-----+ 300
AGCGCGGTACCTCGCGCCATGGGTTGGTCGAGGTTCTCGTTTTTCATATTCTTCGAAtAa

T A I Q A N A T D F K G K Y A F L K T Y 120
ACGGCGATCCAGGCCAATGCCACCGACTTCAAGGGCAAGTAcGCCTTTTTGAAGACGTAC
301 -----+-----+-----+-----+-----+ 360
TGCCGCTAGGTCCGGTTACGGTGGCTGAAGTTCCCGTTCAtgCGGAAAACTTCTGCATG

N Y T L G A D D L T P F G E Q Q L V N S 140
AACTATACTCTGGGTGCGGATGACCTCACTCCCTTTGGGGAGCAGCAGCTGGTGAACCTCG
361 -----+-----+-----+-----+-----+ 420
TTGATATGAGACCCACGCCTACTGGAGTGAGGGAAACCCCTCGTCGTCGACCACCTTGAGC

G I K F Y Q R Y K A L A R S V V P F I R 160
GGCATCAAGTTCTACCAGAGGTACAAGGCTCTGGCGCGCAGTGTTGGTGCCGTTTATTTCGC
421 -----+-----+-----+-----+-----+ 480
CCGTAGTTCAAGATGGTCTCCATGTTCCGAGACCGCGCGTCACACCACGGCAAATAAGCG

A S G S D R V I A S G E K F I E G F Q Q 180
GCCTCAGGCTCGGACCGGGTTATTGCTTCGGGAGAGAAGTTTCATCGAGGGGTTCCAGCAG
481 -----+-----+-----+-----+-----+ 540
CGGAGTCCGAGCCTGGCCCAATAACGAAGCCCTCTCTTCAAGTAGCTCCCCAAGGTCGTC

A K L A D P G A T N R A A P A I S V I I 200
GCGAAGCTGGCTGATCCTGGCGCGACGAACCGCGCCGCTCCGGCGATTAGTGTGATTATT
541 -----+-----+-----+-----+-----+ 600
CGCTTCGACCGACTAGGACCGCGCTGCTTGGCGCGGCGAGGCCGCTAATCACACTAATAA

P E S E T F N N T L D H G V C T K F E A 220
CCGGAGAGCGAGACGTTCAACAATACGCTGGACCACGGTGTGTGCACGAAGTTTGAGGCG
601 -----+-----+-----+-----+-----+ 660
GGCCTCTCGCTCTGCAAGTTGTTATGCGACCTGGTGCCACACACGTGCTTCAAACCTCCGC

Fig. 9a

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```

S Q L G D E V A A N F T A L F A P D I R 240
AGTCAGCTGGGAGATGAGGTTGCGGCCAATTTCACTGCGCTCTTTGCACCCGACATCCGA
661 -----+-----+-----+-----+-----+-----+ 720
TCAGTCGACCCTCTACTCCAACGCCGTTAAAGTGACGCGAGAAACGTGGGCTGTAGGCT

A R L E K H L P G V T L T D E D V V S L 260
GCTCGCctCGAGAAGCATCTTCTGGCGTGACGCTGACAGACGAGGACGTTGTCACTCTA
721 -----+-----+-----+-----+-----+-----+ 780
CGAGCGgaGCTCTTCGTAGAAGGACCGCACTGCGACTGTCTGCTCCTGCAACAGTCAGAT

M D M C P F D T V A R T S D A S Q L S P 280
ATGGACATGTGTcCGTTTGATACGGTAGCGCGCACCAGCGACGCAAGTCAGCTGTCAACCg
781 -----+-----+-----+-----+-----+-----+ 840
TACCTGTACACAgGCAAACCTATGCCATCGCGCGTGGTCGCTGCGTTCACTCGACAGTGGC

F C Q L F T H N E W K K Y D Y L Q S L G 300
TTCTGTCAACTCTTCACTCACAATGAGTGGAAGAAGTACgACTACCTTCAGTCCTTGGGC
841 -----+-----+-----+-----+-----+-----+ 900
AAGACAGTTGAGAAGTGAGTGTTACTCACCTTCTTCATGcTGATGGAAGTCAGGAACCCG

K Y Y G Y G A G N P L G P A Q G I G F T 320
AAGTACTACGGCTACGGCGCAGGCAACCTCTGGGACCGGCTCAGGGGATAGGGTTCAAC
901 -----+-----+-----+-----+-----+-----+ 960
TTCATGATGCCGATGCCGCGTCCGTTGGGAGACCCTGGCCGAGTCCCCTATCCCAAGTGG

N E L I A R L T R S P V Q D H T S T N S 340
AACGAGCTGATTGCCCGGTTGACgCGTTCGCCAGTGCAGGACCACACCAGCACTAACTCG
961 -----+-----+-----+-----+-----+-----+ 1020
TTGCTCGACTAACGGGCCAACTGcGCAAGCGGTCACGTCCTGGTGTGGTCGTGATTGAGC

T L V S N P A T F P L N A T M Y V D F S 360
ACTCTAGTCTCCAACCCGGCCACCTTCCCGTTGAACGCTACCATGTACGTCGACTTTTCA
1021 -----+-----+-----+-----+-----+-----+ 1080
TGAGATCAGAGGTTGGGCCGGTGAAGGGCAACTTGCGATGGTACATGCAGCTGAAAAGT

H D N S M V S I F F A L G L Y N G T E P 380
CACGACAACAGCATGGTTTCCATCTTCTTTGCATTGGGCCTGTACAACGGCACTGAACCC
1081 -----+-----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGCTACCAAAGGTAGAAGAAACGTAACCCGGACATGTTGCCGTGACTTGGG

L S R T S V E S A K E L D G Y S A S W V 400
TTGTCCCGGACCTCGGTGGAAGCGCCAAGGAATTGGATGGGTATTCTGCATCCTGGGTG
1141 -----+-----+-----+-----+-----+-----+ 1200
AACAGGGCCTGGAGCCACCTTTCGCGGTTCCCTTAACCTACCCATAAGACGTAGGACCCAC

V P F G A R A Y F E T M Q C K S E K E P 420
GTGCCTTTTCGGCGCGGAGCCTACTTCGAGACGATGCAATGCAAGTCGGAAGAGGAGCCT
1201 -----+-----+-----+-----+-----+-----+ 1260
CACGGAAGCCGCGCGCTCGGATGAAGCTCTGCTACGTTACGTTACGCTTTTCTCGGA

L V R A L I N D R V V P L H G C D V D K 440
CTTGTTTCGCGCTTTGATTAATGACCGGTTGTGCCACTGCATGGCTGCGATGTGGACAAG
1261 -----+-----+-----+-----+-----+-----+ 1320
GAACAAGCGCGAAACTAATTACTGGCCCAACACGGTGACGTACCGACGCTACACCTGTTC

```

Fig. 9b

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```
      L G R C K L N D F V K G L S W A R S G G      460
      CTGGGGCGATGCAAGCTGAATGACTTTGTCAAGGGATTGAGTTGGGCCAGATCTGGGGGC
1321 -----+-----+-----+-----+-----+-----+ 1380
      GACCCCGCTACGTTCGACTTACTGAAACAGTTCCTAACTCAACCCGGTCTAGACCCCG

      N W G E C F S *      467
      AACTGGGGAGAGTGCTTTAGTTGA
1381 -----+-----+----- 1404
      TTGACCCTCTCACGAAATCAACT
```

Fig. 9c

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CP-1
 Eco RI M G V F V V L L S I A T L F G S T
 TATATGAATTCATGGGCGTGTTCGTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCA
 1 -----+-----+-----+-----+-----+-----+ 60
 ATATACTTAAGTACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGT

 S G T A L G P R G N S H S C D T V D G G
 CATCCGGTACCGCCTTGGGTCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTG
 61 -----+-----+-----+-----+-----+-----+ 120
 GTAGGCCATGGCGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACCTGCCAC
 CP-2
 CP-3
 Y Q C F P E I S H L W G Q Y S P Y F S L
 GTTACCAATGTTTCCCAGAAATTTCTCACTTGTGGGGTCAATACTCTCCATACTTCTCTT
 121 -----+-----+-----+-----+-----+-----+ 180
 CAATGGTTACAAAGGGTCTTTAAAGAGTGAACACCCAGTTATGAGAGGTATGAAGAGAA

 E D E S A I S P D V P D D C R V T F V Q
 TGAAGACGAATCTGCTATTTCTCCAGACGTTCCAGACGACTGTAGAGTTACTTTTCGTTT
 181 -----+-----+-----+-----+-----+-----+ 240
 ACCTTCTGCTTAGACGATAAAGAGGTCTGCAAGGTCTGCTGACATCTCAATGAAAGCAAG
 CP-4.7
 CP-5.7
 V L S R H G A R Y P T D S K G K K Y S A
 AAGTTTTGTCTAGACACGGTGCTAGATACCCAACTgacTCTAAGggtAAGaagTACTCTG
 241 -----+-----+-----+-----+-----+-----+ 300
 TTCAAAACAGATCTGTGCCACGATCTATGGGTGActgAGATTCCAATTCTtcATGAGAC

 L I E A I Q K N A T A F K G K Y A F L K
 CTTTGATTGAAGCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGA
 301 -----+-----+-----+-----+-----+-----+ 360
 GAAACTAAGTTTCTGCGATGACGAAAGTTCCCATTCATGCGAAAGAACT
 CP-6
 CP-7
 T Y N Y T L G A D D L T P F G E N Q M V
 AGACTTACAACCTACACTTTGGGTGCTGACGACTTGACTCCATTGCGGTGAAAACCAATGG
 361 -----+-----+-----+-----+-----+-----+ 420
 TCTGAATGTTGATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACC

 N S G I K F Y R R Y K A L A R K I V P F
 TTAAGTCTGGTATTAAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCAT
 421 -----+-----+-----+-----+-----+-----+ 480
 AATTGAGACCATAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTA
 CP-8.7
 CP-9
 I R A S G S S R V I A S A E K F I E G F
 TCATTAGAGCTTCTGGTTCTtctAGAGTTATTGCTTCTGCTGAAAAGTTCAATTGAAGGTT
 481 -----+-----+-----+-----+-----+-----+ 540
 AGTAATCTCGAAGACCAAGAgaTCTCAATAACGAAGACGACTTTTCAAGTAACCTCCAA

 Q S A K L A D P G S Q P H Q A S P V I D
 TCCAATCTGCTAAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTG
 541 -----+-----+-----+-----+-----+-----+ 600
 AGGTTAGACGATTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTCTGAAGAGGTCAATAAC

Fig. 10a

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CP-10.7

CP-11.7

V I I S E A S S Y N N T L D P G T C T A
 ACGTTATTATTtctGACgctTCTtctTACAACAACACTTTGGACccaGGTACTTGTACTG
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 TGCAATAATAAagaCTgcgaAGGagaATGTTGTTGTGAAACCTGggtCCATGAACATGAC

F E D S E L A D T V E A N F T A L F A P
 CTTTCGAAGACTCTGAATTGgctGACactGTTGAAGCTAACTTCACTGCTTTGTTGCTC
 661 -----+-----+-----+-----+-----+-----+ 720
 GAAAGCTTCTGAGACTTAACcgaCTGtgaCAACTTCGATTGAAGTGACGAAACAAGCGAG

CP-12.7

A I R A R L E A D L P G V T L T D T E V
 CAGCTATTAGAGCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACactgaaG
 721 -----+-----+-----+-----+-----+-----+ 780
 GTCGATAATCTCGATCTAACCTTCGACTGAACGGTCCACAATGAAACTGACTGtgacttc

CP-13.7

T Y L M D M C S F E T V A R T S D A T E
 TTactTACTTGATGGACATGTGTtctTTTCGAAACTGTTGCTAGAACTTCTGACGCTACTG
 781 -----+-----+-----+-----+-----+-----+ 840
 AatgaATGAACTACCTGTACACAagaAAGCTTTGACAACGATCTTGAAGACTGCGATGAC

L S P F C A L F T H D E W R H Y D Y L Q
 AATTGTCTCCATTCTGTGCTTTGTTCACTCAGACGAATGGAGAcactTACGACTACTTGC
 841 -----+-----+-----+-----+-----+-----+ 900
 TTAACAGAGGTAAGACACGAAACAAGTGAGTGCTGCTTACCTCTgtgATGCTGATGAACG

CP-14.7

CP-15.7

S L K K Y Y G H G A G N P L G P T Q G V
 AATCTTTGaagAAGTACTACGGTcacGGTGCTGTTAACCCATTGGGTCCAactCAAGGTG
 901 -----+-----+-----+-----+-----+-----+ 960
 TTAGAAACttctTTCATGATGCCagtGCCACGACCATTGGGTAAACCCAGGTtgaGTTCCAC

G F A N E L I A R L T R S P V Q D H T S
 TTGGTTTCGCTAACGAATTGATTGCTAGATTGACTAGATCTCCAGTTCAAGACCACACTT
 961 -----+-----+-----+-----+-----+-----+ 1020
 AACCAAAGCGATTGCTTAACTAACGATCTAACTGATCTAGAGGTCAAGTTCTGGTGTGAA

CP-16

CP-17.7

T N H T L D S N P A T F P L N A T L Y A
 CTACTAACCCACACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACG
 1021 -----+-----+-----+-----+-----+-----+ 1080
 GATGATTGGTGTGAAACCTGAGATTGGGTGCGATGAAAGGGTAACCTGCGATGAAACATGC

D F S H D N G I I S I F F A L G L Y N G
 CTGACTTCTCTCACGACAACggtattATTCTATTTCTTCGCTTTGGGTTTGTACAACG
 1081 -----+-----+-----+-----+-----+-----+ 1140
 GACTGAAGAGAGTGCTGTTGccataaTAAAGATAAAAGAAGCGAAACCCAAACATGTTGC

CP-18.7

CP-19.7

T A P L S T T S V E S I E E T D G Y S S
 GTACTGCTCCATTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTt
 1141 -----+-----+-----+-----+-----+-----+ 1200
 CATGACGAGGTAACAGATGATGAAGACAACCTTAGATAACTTCTTTGACTGCCAATGAGAA

Fig. 10b

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A W T V P F A S R A Y V E M M Q C Q A E
ctgctTGGACTGTTCCATTGccttctAGAGCTTACGTTGAAATGATGCAATGTCAAGCTG
1201 -----+-----+-----+-----+-----+-----+ 1260
gacgaACCTGACAAGGTAAGcgaagaTCTCGAATGCAACTTTACTACGTTACAGTTCGAC
CP-20
CP-21
K E P L V R V L V N D R V V P L H G C A
AAAAGGAACCATTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTG
1261 -----+-----+-----+-----+-----+ 1320
TTTTCTTGGTAAACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACAC
V D K L G R C K R D D F V E G L S F A R
CTGTTGACAAGTTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTA
1321 -----+-----+-----+-----+-----+ 1380
GACAACTGTTCAACCCATCTACATTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGAT
CP-22
S G G N W A E C F A * Eco RI
GATCTGGTGGTAACTGGGCTGAATGTTTCGCTTAAGAATTCATATA
1381 -----+-----+-----+-----+----- 1426
CTAGACCACCATTGACCCGACTTACAAAGCGAATTCTTAAGTATAT

Fig. 10c

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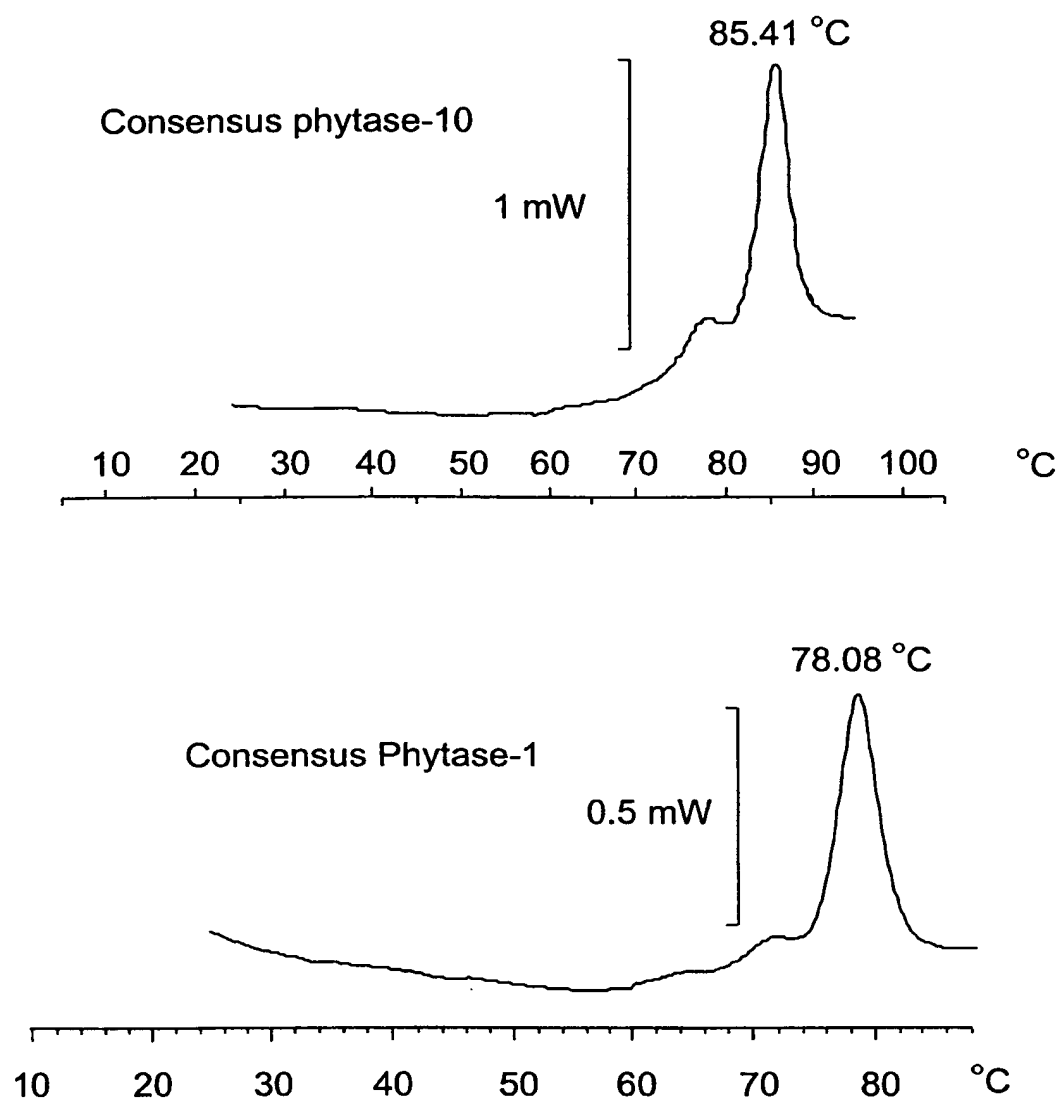


Fig. 11

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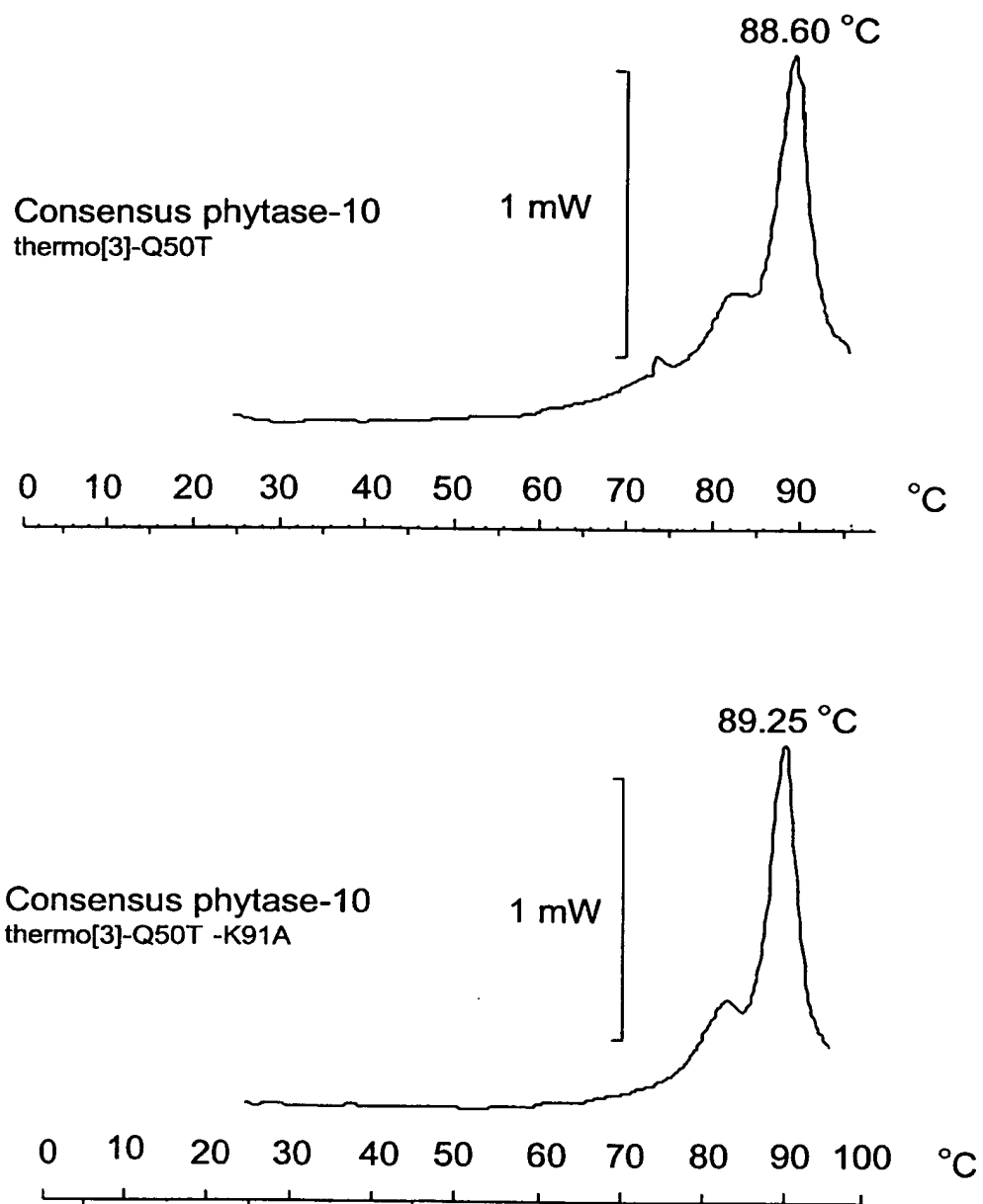


Fig. 12

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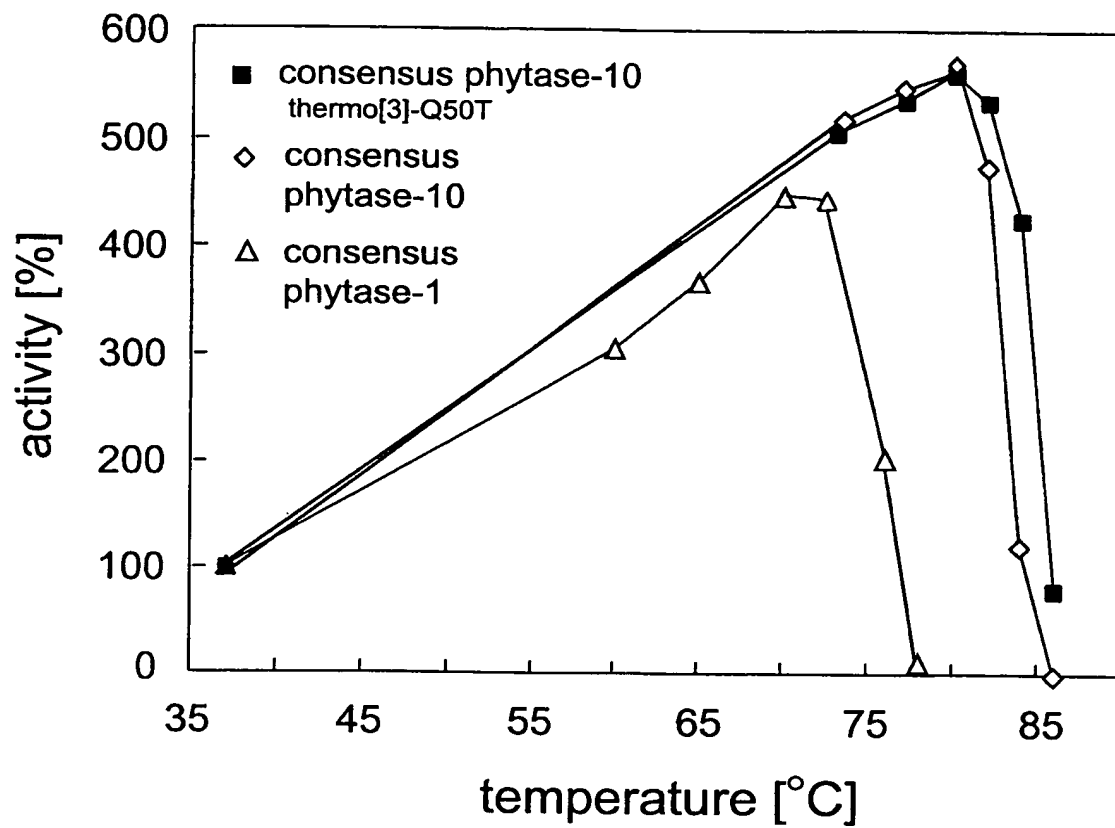


Fig. 13

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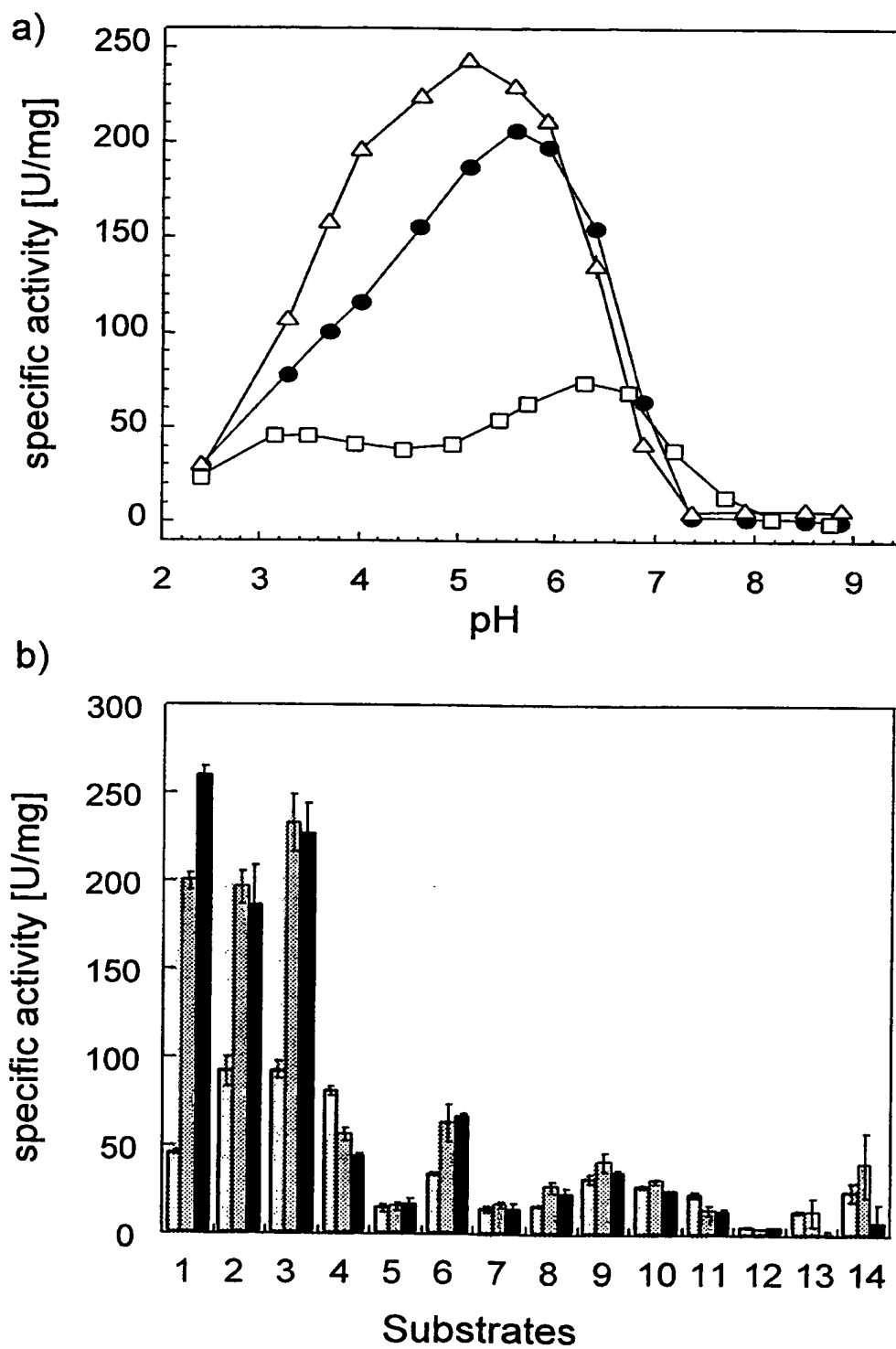


Fig. 14

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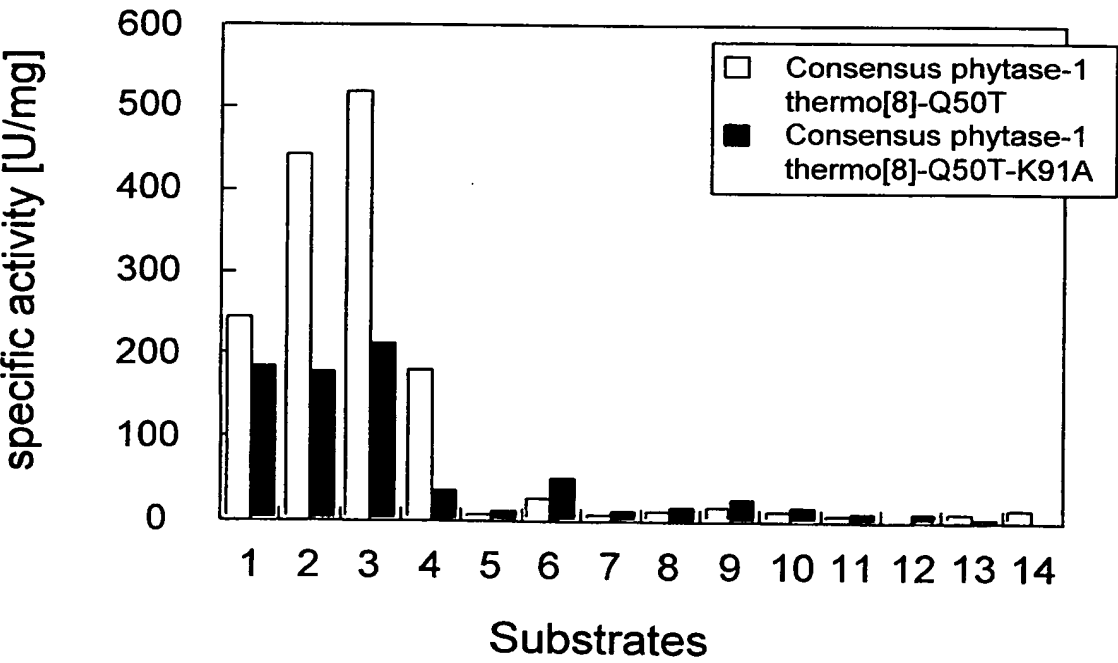
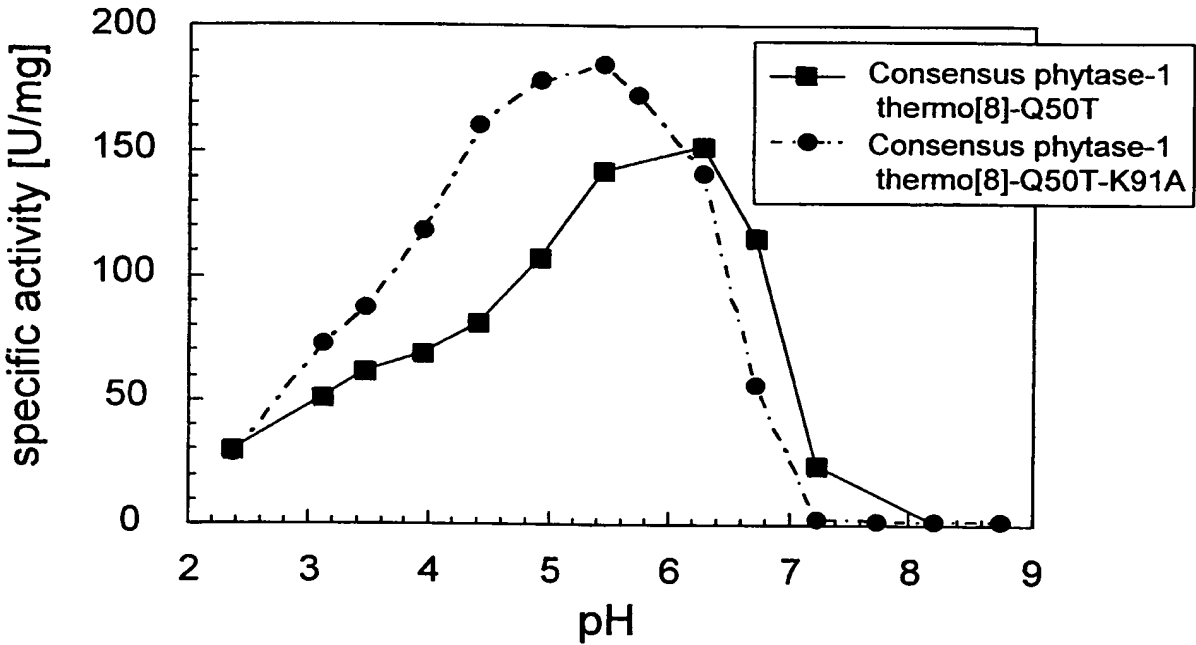


Fig. 15

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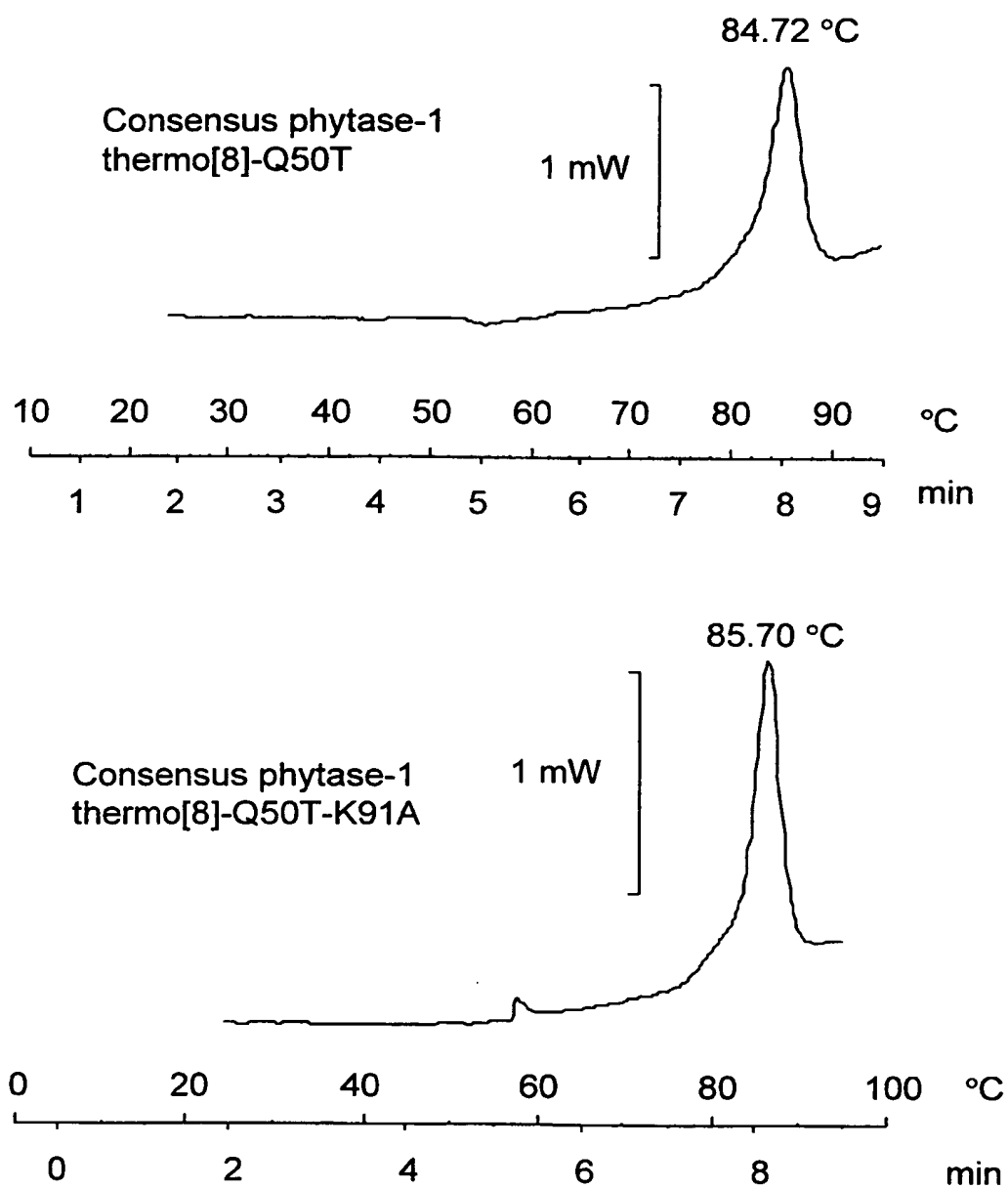


Fig. 16

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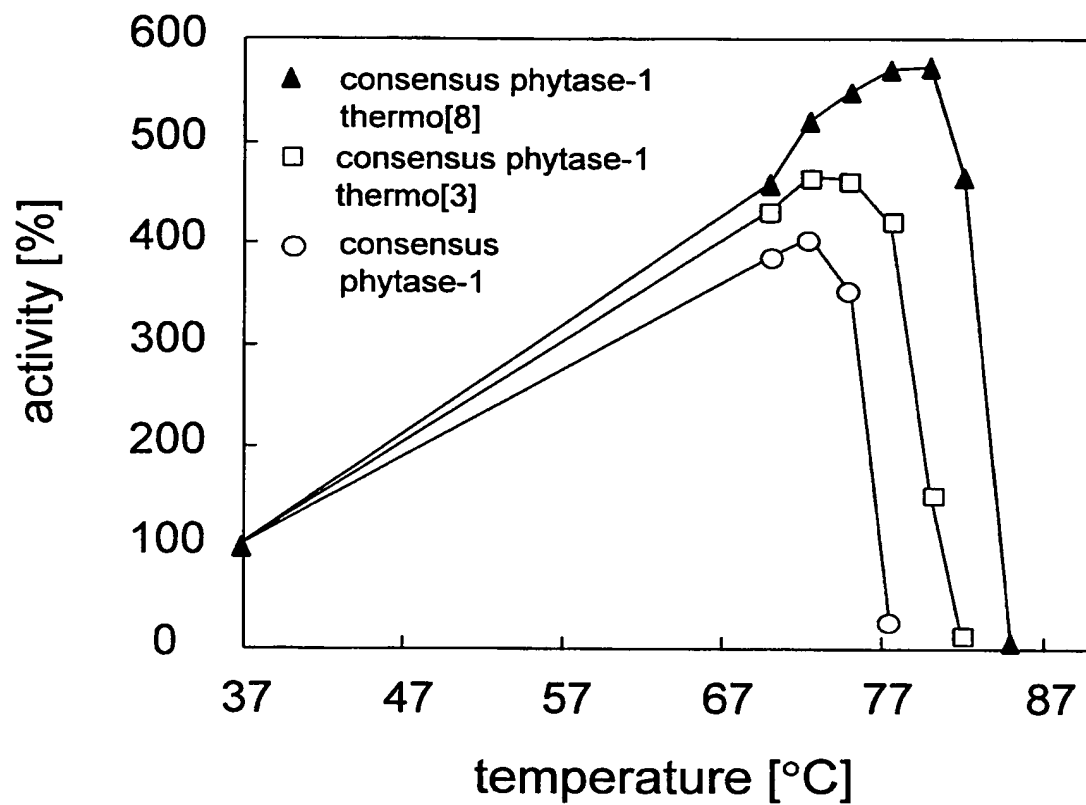


Fig. 17

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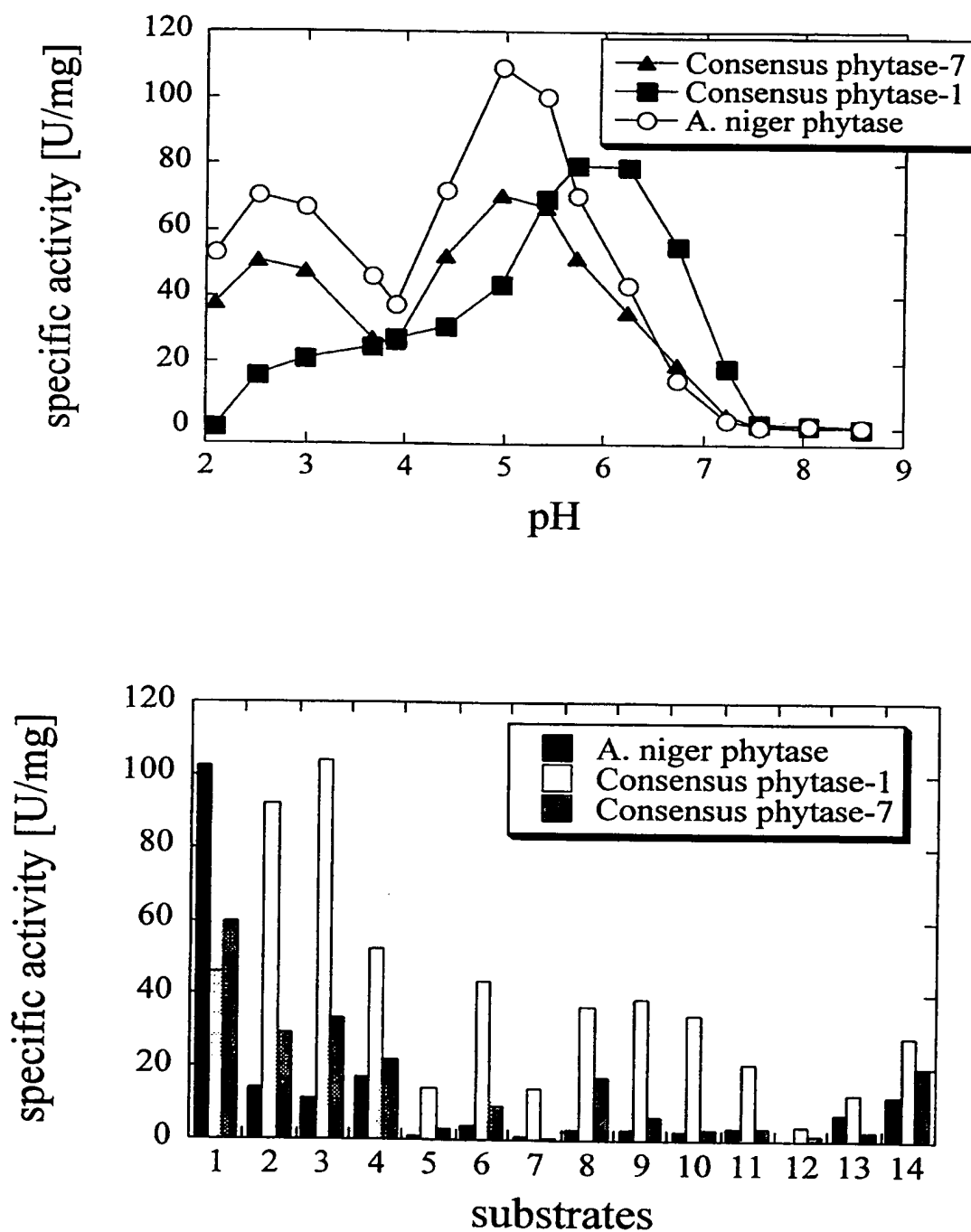


Fig. 18

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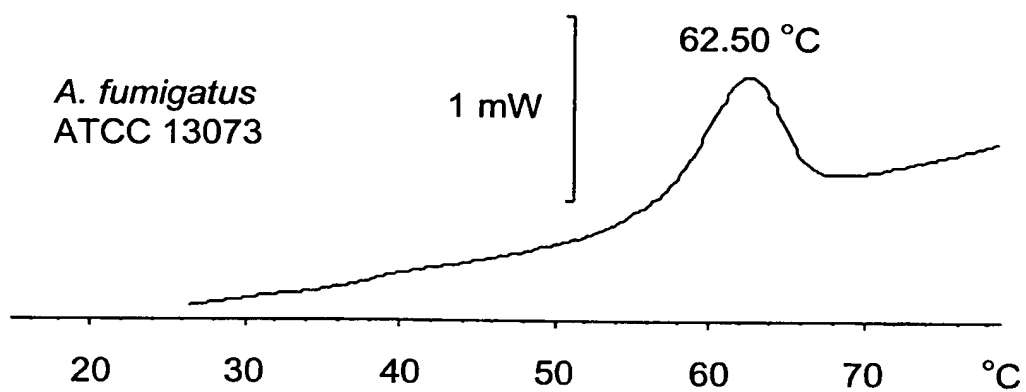
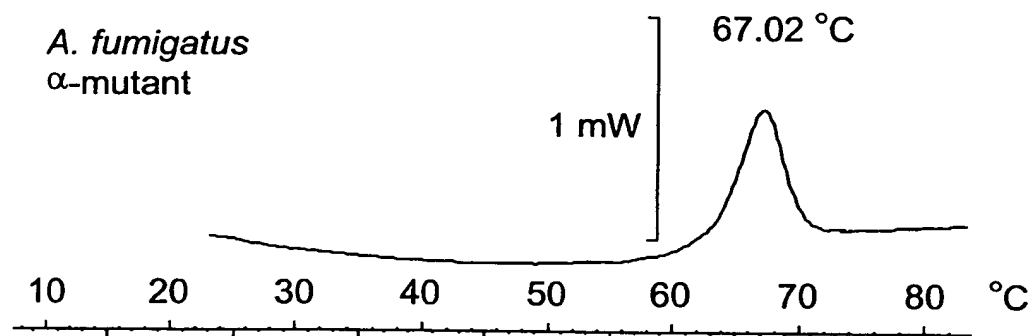


Fig. 19

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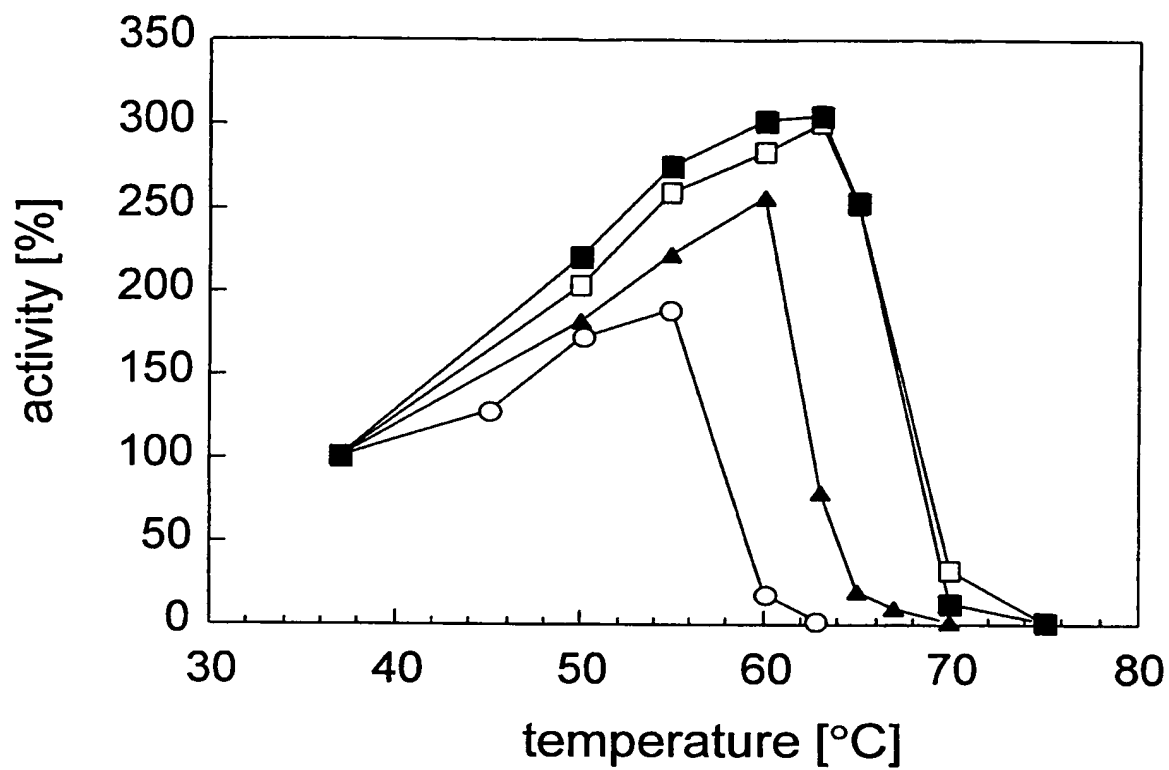


Fig. 20

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1 MGVFVLLSI ATLFGSTSGT ALGPRGNSHS CDTVDGGYQC FPEISSNWSP
51 YSPYFSLADE SAISPDVPKG CRVTFVQVLQ RHGARFPTSG AATRISALIE
101 AIQKNATAFK GKYAFLKTYN YTLGADDLVP FGANQSSQAG IKFYRRYKAL
151 ARKIVPFIRA SGSDRVIDSA TNWIEGFQSA KLADPGANPH QASPVINVII
201 PEGAGYNNTL DHGLCTAFEE SELGDDVEAN FTAVFAPPIR ARLEAHLPGV
251 NLTDDEVVNL MDMCPFDIVA RTSDATELSP FCDLFTHDEW IQYDYLGDLD
301 KYYGTGAGNP LGPAQGVGFV NELIARLTHS PVQDHTSTNH TLDSNPATFP
351 LNATLYADFS HDNTMVAIFF ALGLYNGTKP LSTTSVESIE ETDGYSASWL
401 VPFSARMYVE MMQCEAEKEP LVRVLVNDRV VPLHGCGVDK LGRCKRDDFV
451 EGLSFARSGG NWEECFA

Fig. 21

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```

ATGGGCGTGTTTCGTCTGCTACTGTCCATTGCCACCTTGTTTCGGTTCACATCCGGTACC
1  -----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGTAGGCCATGG

M G V F V V L L S I A T L F G S T S G T -

GCCTTGGGTCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61 -----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

A L G P R G N S H S C D T V D G G Y Q C -

TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
121 -----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

F P E I S H L W G T Y S P Y F S L A D E -

TCTGCTATTTCTCCAGACGTCCCAAAGGACTGTAGAGTTACTTTTCGTTCAAGTTTGTCT
181 -----+-----+-----+-----+-----+-----+ 240
AGACGATAAAGAGGTCTGCAGGGTTTCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

S A I S P D V P K D C R V T F V Q V L S -

AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGGCTTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTTGAAGAAGATTTCAGATTCCGAATGAGACGAAACTAAGTT

R H G A R Y P T S S K S K A Y S A L I E -

GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301 -----+-----+-----+-----+-----+-----+ 360
CGATAAGTTTCTTGCATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

A I Q K N A T A F K G K Y A F L K T Y N -

TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAAAACCAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+ 420
ATGTGAAAACCCACGACTGCTGAACTGAGGTAAAGCCACTTTTGGTTTACCAATTGAGACCA

Y T L G A D D L T P F G E N Q M V N S G -

ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTTCATTAGAGCT
421 -----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

I K F Y R R Y K A L A R K I V P F I R A -

TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

S G S D R V I A S A E K F I E G F Q S A -

```

Fig. 22a

46/56

AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
541 -----+-----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTTCGAAGAGGTCAATAATTGCACTAGTAA

K L A D P G S Q P H Q A S P V I N V I I -

CCAGAAGGATCCGGTTACAACAACACTTTGGACCATGGTCTTTGTACTGCTTTTGAAGAC
601 -----+-----+-----+-----+-----+-----+ 660
GGTCTTCCTAGGCCAATGTTGTGTGAAACCTGGTACCAGAAACATGACGAAAGCTTCTG

P E G S G Y N N T L D H G L C T A F E D -

TCTACCCTAGGTGACGACGTTGAAGCTAACTTCAGTCTTTGTTCGCTCCAGCTATTAGA
661 -----+-----+-----+-----+-----+-----+ 720
AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTGATAATCT

S T L G D D V E A N F T A L F A P A I R -

GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG
721 -----+-----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGACTGAACGGTCCACAATGAACTGACTGCTTCTGCAACAAATGAAC

A R L E A D L P G V T L T D E D V V Y L -

ATGGACATGTGTCCATTTCGACACTGTGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
781 -----+-----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAGCGATCTTGAAGACTGCGATGACTTAACAGAGGT

M D M C P F D T V A R T S D A T E L S P -

TTCTGTGCTTTGTTCACTCAGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
841 -----+-----+-----+-----+-----+-----+ 900
AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTTTCGAACCCA

F C A L F T H D E W I Q Y D Y L Q S L G -

AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT
901 -----+-----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTTGGTAACCCAGGTTCGAGTTCCACAACCAAAGCGA

K Y Y G Y G A G N P L G P A Q G V G F A -

AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+-----+ 1020
TTGCTTAACCTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

N E L I A R L T H S P V Q D H T S T N H -

ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

T L D S N P A T F P L N A T L Y A D F S -

Fig. 22b

47/56

```
CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081 -----+-----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACTATAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

H D N T M I S I F F A L G L Y N G T K P -

TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT
1141 -----+-----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

L S T T S V E S I E E T D G Y S A S W T -

GTTCCATTTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

V P F A A R A Y V E M M Q C Q A E K E P -

TTGGTTAGAGTTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+-----+ 1320
AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACCTGTTT

L V R V L V N D R V V P L H G C A V D K -

TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

L G R C K R D D F V E G L S F A R S G G -

AACTGGGCTGAATGTTTCGCTTAA
1381 -----+-----+----- 1404
TTGACCCGACTTACAAAGCGAATT

N W A E C F A *
```

Fig. 22c

48/56

```
ATGGGCGTGTTTCGTCTGCTACTGTCCATTGCCACCTTGTTTCGGTTCACATCCGGTACC
1  -----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGTAGGCCATGG

M G V F V V L L S I A T L F G S T S G T -

GCCTTGGGTCTCTGCTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61  -----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

A L G P R G N S H S C D T V D G G Y Q C -

TTCCCAGAAATTTCTCACTTGTGGGGTACCTACTCTCCATACTTCTCTTTGGCAGACGAA
121 -----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTTAAAGAGTGAACACCCCATGGATGAGAGGTATGAAGAGAAACCGTCTGCTT

F P E I S H L W G T Y S P Y F S L A D E -

TCTGCTATTTCTCCAGACGTCCCAAAGGACTGTAGAGTTACTTTTCGTTCAAGTTTTGTCT
181 -----+-----+-----+-----+-----+-----+ 240
AGACGATAAAGAGGTCTGCAGGGTTTCCTGACATCTCAATGAAAGCAAGTTCAAAACAGA

S A I S P D V P K D C R V T F V Q V L S -

AGACACGGTGCTAGATACCCAATTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAACTAATT

R H G A R Y P T S S A S K A Y S A L I E -

GCTATTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC
301 -----+-----+-----+-----+-----+-----+ 360
CGATAAGTTTTCTTGCATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTG

A I Q K N A T A F K G K Y A F L K T Y N -

TACACTTTGGGTGCTGACGACTTGACTCCATTTCGGTGAAAACCAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+ 420
ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTTTGGTTTACCAATTGAGACCA

Y T L G A D D L T P F G E N Q M V N S G -

ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTCTAGAGCT
421 -----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

I K F Y R R Y K A L A R K I V P F I R A -

TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGACTTTTCAAGTAACTTCCAAAGGTTAGACGA

S G S D R V I A S A E K F I E G F Q S A -
```

Fig. 23a

49/56

AAGTTGGCTGACCCAGGTTCTCAACCACACCAAGCTTCTCCAGTTATTAACGTGATCATT
541 -----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCAAGAGTTGGTGTGGTTTGAAGAGGTCAATAATTGCACTAGTAA
K L A D P G S Q P H Q A S P V I N V I I -
CCAGAAGGATCCGGTTACAACAACACTTTGGACCATGGTCTTTGTACTGCTTTTGAAGAC
601 -----+-----+-----+-----+-----+ 660
GGTCTTCCTAGGCCAATGTTGTTGTGAAACCTGGTACCAGAAACATGACGAAAGCTTCTG
P E G S G Y N N T L D H G L C T A F E D -
TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTTTGTTTCGCTCCAGCTATTAGA
661 -----+-----+-----+-----+-----+ 720
AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGAAACAAGCGAGGTGATAATCT
S T L G D D V E A N F T A L F A P A I R -
GCTAGATTGGAAGCTGACTTGCCAGGTGTTACTTTGACTGACGAAGACGTTGTTTACTTG
721 -----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGACTGAACGGTCCACAATGAACTGACTGCTTCTGCAACAAATGAAC
A R L E A D L P G V T L T D E D V V Y L -
ATGGACATGTGTCCATTTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATTGTCTCCA
781 -----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAGCGATCTTGAAGACTGCGATGACTTAACAGAGGT
M D M C P F D T V A R T S D A T E L S P -
TTCTGTGCTTTGTTCACTCACGACGAATGGATCCAATACGACTACTTGCAAAGCTTGGGT
841 -----+-----+-----+-----+-----+ 900
AAGACACGAAACAAGTGAGTGCTGCTTACCTAGGTTATGCTGATGAACGTTTGAACCCA
F C A L F T H D E W I Q Y D Y L Q S L G -
AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGCT
901 -----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCGA
K Y Y G Y G A G N P L G P A Q G V G F A -
AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+ 1020
TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG
N E L I A R L T H S P V Q D H T S T N H -
ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGCGATGAAAGGGTAAGTTGCGATGAAACATGCGACTGAAGAGA
T L D S N P A T F P L N A T L Y A D F S -

Fig. 23b

50/56

```
CACGACAACACTATGATATCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACCAAGCCA
1081 -----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACTATAGATAAAAAGAAGCGAAACCCAAACATGTTGCCATGGTTCGGT

H D N T M I S I F F A L G L Y N G T K P -

TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT
1141 -----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTTAGATAAAGTTCTTTGACTGCCAATGAGACGAAGAACCTGA

L S T T S V E S I E E T D G Y S A S W T -

GTTCCATTTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACAGTTCGACTTTTCCTTGGT

V P F A A R A Y V E M M Q C Q A E K E P -

TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+ 1320
AACCAATCTCAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACCTGTTC

L V R V L V N D R V V P L H G C A V D K -

TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

L G R C K R D D F V E G L S F A R S G G -

AACTGGGCTGAATGTTTCGCTTAA
1381 -----+-----+----- 1404
TTGACCCGACTTACAAAGCGAATT

N W A E C F A *
```

Fig. 23c

51/56

```
ATGGGCGTGTTTCGTGCTACTGTCCATTGCCACCTTGTTCGGTTCCACATCCGGTACC
1  -----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCACGATGACAGGTAACGGTGGAACAAGCCAAGGTGTAGGCCATGG

M G V F V V L L S I A T L F G S T S G T -

GCCTTGGGTCCTCGTGGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61  -----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTAAAGAGTGAGAACACTGTGACAACTGCCACCAATGGTTACA

A L G P R G N S H S C D T V D G G Y Q C -

TTCACAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA
121 -----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTTAAAGAGTGAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

F P E I S H L W G T Y S P F F S L A D E -

TCTGCTATTTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTCGTTCAAGTTTTGTCT
181 -----+-----+-----+-----+-----+-----+ 240
AGACGATAAAGAGGTCTGCAAGGTTTCCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

S A I S P D V P K G C R V T F V Q V L S -

AGACACGGTGCTAGATACCCAACTTCTTCTAAGTCTAAGGCTTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTGAAGAAGATTTCAGATTCCGAATGAGACGAACTAACTT

R H G A R Y P T S S K S K A Y S A L I E -

GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAT
301 -----+-----+-----+-----+-----+-----+ 360
CGATAAGTTTTCTTGCATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTA

A I Q K N A T A F K G K Y A F L K T Y N -

TACACTTTGGGTGCTGACGACTTGACTCCATTCCGGTGAACAACAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+ 420
ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTTGTTTACCAATTGAGACCA

Y T L G A D D L T P F G E Q Q M V N S G -

ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTTCATTAGAGCT
421 -----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

I K F Y R R Y K A L A R K I V P F I R A -

TCTGGTTCTGACAGAGTTATTGCTTCTGCCGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGGCTTTTCAAGTAACTTCCAAAGGTTAGACGA

S G S D R V I A S A E K F I E G F Q S A -
```

Fig. 24a

52/56

AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
541 -----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCACGATTGGGTGTGGTTTGAAGAGGTCAATAATTGCAATAATAA

K L A D P G A N P H Q A S P V I N V I I -

CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTCGAAGAA
601 -----+-----+-----+-----+-----+ 660
GGTCTTCCACGACCAATGTTGTTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

P E G A G Y N N T L D H G L C T A F E E -

TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTTCGCTCCACCAATTAGA
661 -----+-----+-----+-----+-----+ 720
AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

S T L G D D V E A N F T A V F A P P I R -

GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTAACTTG
721 -----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

A R L E A H L P G V N L T D E D V V N L -

ATGGACATGTGTCCATTTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
781 -----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

M D M C P F D T V A R T S D A T Q L S P -

TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
841 -----+-----+-----+-----+-----+ 900
AAGACACTGAACAAGTGAGTGCTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

F C D L F T H D E W I Q Y D Y L Q S L G -

AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
901 -----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTTGGGTAACCCAGGTTCGAGTTCCACAACCAAAGCAA

K Y Y G Y G A G N P L G P A Q G V G F V -

AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+ 1020
TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

N E L I A R L T H S P V Q D H T S T N H -

ACTTTGGACTCTAACCCAGCTACTTTCCCATTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGCGATGAAAGGGTAACTTGCGATGAAACATGCGACTGAAGAGA

T L D S N P A T F P L N A T L Y A D F S -

Fig. 24b

53/56

```
CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
1081 -----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCGGT

H D N T M V S I F F A L G L Y N G T K P -

TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGA
1141 -----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTTAGATAAATTCTTTGACTGCCAATGAGACGAAGAACCTGA

L S T T S V E S I E E T D G Y S A S W T -

GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCTTGGT

V P F A A R A Y V E M M Q C E A E K E P -

TTGGTTAGAGTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+ 1320
AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACCTGTT

L V R V L V N D R V V P L H G C A V D K -

TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

L G R C K R D D F V E G L S F A R S G G -

AACTGGGAAGAATGTTTCGCTTAA
1381 -----+-----+----- 1404
TTGACCCTTCTTACAAAGCGAATT

N W E E C F A *
```

Fig. 24c

54/56

```
ATGGGCGTGTTCGTCTGCTACTGTCCATTGCCACCTTGTTTCGGTTCACATCCGGTACC
1  -----+-----+-----+-----+-----+-----+ 60
TACCCGCACAAGCAGCACGATGACAGGTAACGGTGAACAAGCCAAGGTGTAGGCCATGG

M G V F V V L L S I A T L F G S T S G T -

GCCTTGGGTCTCTGTTGTAATTCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT
61  -----+-----+-----+-----+-----+-----+ 120
CGGAACCCAGGAGCACCATTAAGAGTGAGAACACTGTGACAACCTGCCACCAATGGTTACA

A L G P R G N S H S C D T V D G G Y Q C -

TTCCCAGAAATTTCTCACTTGTGGGGTACATACTCTCCATTCTTCTCTTTGGCTGACGAA
121 -----+-----+-----+-----+-----+-----+ 180
AAGGGTCTTTAAAGAGTGAACACCCCATGTATGAGAGGTAAGAAGAGAAACCGACTGCTT

F P E I S H L W G T Y S P F F S L A D E -

TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTTCGTTCAAGTTTGTCT
181 -----+-----+-----+-----+-----+-----+ 240
AGACGATAAAGAGGTCTGCAAGGTTTCCCAACATCTCAATGAAAGCAAGTTCAAAACAGA

S A I S P D V P K G C R V T F V Q V L S -

AGACACGGTGCTAGATACCCAACTTCTTCTGCGTCTAAGGCTTACTCTGCTTTGATTGAA
241 -----+-----+-----+-----+-----+-----+ 300
TCTGTGCCACGATCTATGGGTTGAAGAAGACGCAGATTCCGAATGAGACGAAACTAAGTT

R H G A R Y P T S S A S K A Y S A L I E -

GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAT
301 -----+-----+-----+-----+-----+-----+ 360
CGATAAGTTTCTTTCGATGACGAAAGTTCCCATTCATGCGAAAGAACTTCTGAATGTTA

A I Q K N A T A F K G K Y A F L K T Y N -

TACACTTTGGGTGCTGACGACTTGACTCCATTTCGGTGAACAACAAATGGTTAACTCTGGT
361 -----+-----+-----+-----+-----+-----+ 420
ATGTGAAACCCACGACTGCTGAACTGAGGTAAGCCACTTGTGTGTTACCAATTGAGACCA

Y T L G A D D L T P F G E Q Q M V N S G -

ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTTCATTAGAGCT
421 -----+-----+-----+-----+-----+-----+ 480
TAATTCAAGATGTCTTCTATGTTCCGAAACCGATCTTTCTAACAAGGTAAGTAATCTCGA

I K F Y R R Y K A L A R K I V P F I R A -

TCTGGTTCGACAGAGTTATTGCTTCTGCCGAAAAGTTCATTGAAGGTTTCCAATCTGCT
481 -----+-----+-----+-----+-----+-----+ 540
AGACCAAGACTGTCTCAATAACGAAGACGGCTTTTCAAGTAACTTCCAAAGGTTAGACGA

S G S D R V I A S A E K F I E G F Q S A -
```

Fig. 25a

55/56

AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTATT
541 -----+-----+-----+-----+-----+-----+ 600
TTCAACCGACTGGGTCCACGATTGGGTGTTGTTTGAAGAGGTCAATAATTGCAATAATAA

K L A D P G A N P H Q A S P V I N V I I -

CCAGAAGGTGCTGGTTACAACAACACTTTGGACCACGGTTTGTGTACTGCTTTTGAAGAA
601 -----+-----+-----+-----+-----+-----+ 660
GGTCTTCCACGACCAATGTTGTGTGAAACCTGGTGCCAAACACATGACGAAAGCTTCTT

P E G A G Y N N T L D H G L C T A F E E -

TCTACCCTAGGTGACGACGTTGAAGCTAACTTCACTGCTGTTTTTCGCTCCACCAATTAGA
661 -----+-----+-----+-----+-----+-----+ 720
AGATGGGATCCACTGCTGCAACTTCGATTGAAGTGACGACAAAAGCGAGGTGGTTAATCT

S T L G D D V E A N F T A V F A P P I R -

GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG
721 -----+-----+-----+-----+-----+-----+ 780
CGATCTAACCTTCGAGTGAACGGTCCACAATTGAACTGACTGCTTCTGCAACAATTGAAC

A R L E A H L P G V N L T D E D V V N L -

ATGGACATGTGTCCATTTCGACACTGTTTGCTAGAACTTCTGACGCTACTCAATTGTCTCCA
781 -----+-----+-----+-----+-----+-----+ 840
TACCTGTACACAGGTAAGCTGTGACAACGATCTTGAAGACTGCGATGAGTTAACAGAGGT

M D M C P F D T V A R T S D A T Q L S P -

TTCTGTGACTTGTTCACTCACGACGAATGGATTCAATACGACTACTTGCAATCTTTGGGT
841 -----+-----+-----+-----+-----+-----+ 900
AAGACACTGAACAAGTGAGTGCTTGCTTACCTAAGTTATGCTGATGAACGTTAGAAACCCA

F C D L F T H D E W I Q Y D Y L Q S L G -

AAGTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCGTT
901 -----+-----+-----+-----+-----+-----+ 960
TTCATGATGCCAATGCCACGACCATTTGGGTAACCCAGGTCGAGTTCCACAACCAAAGCAA

K Y Y G Y G A G N P L G P A Q G V G F V -

AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACTAACCAC
961 -----+-----+-----+-----+-----+-----+ 1020
TTGCTTAACTAACGATCTAACTGAGTGAGAGGTCAAGTTCTGGTGTGAAGATGATTGGTG

N E L I A R L T H S P V Q D H T S T N H -

ACTTTGGACTCTAACCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT
1021 -----+-----+-----+-----+-----+-----+ 1080
TGAAACCTGAGATTGGGTGCGATGAAAGGGTAACCTGCGATGAAACATGCGACTGAAGAGA

T L D S N P A T F P L N A T L Y A D F S -

Fig. 25b

56/56

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CACGACAACACTATGGTTTCTATTTTCTTCGCTTTGGGTTTGTACAACGGTACTAAGCCA
1081 -----+-----+-----+-----+-----+ 1140
GTGCTGTTGTGATACCAAAGATAAAAGAAGCGAAACCCAAACATGTTGCCATGATTCCGGT

H D N T M V S I F F A L G L Y N G T K P -

TTGTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT
1141 -----+-----+-----+-----+-----+ 1200
AACAGATGATGAAGACAACCTTAGATAACTTCTTTGACTGCCAATGAGACGAAGAACCTGA

L S T T S V E S I E E T D G Y S A S W T -

GTTCCATTTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCA
1201 -----+-----+-----+-----+-----+ 1260
CAAGGTAAGCGACGATCTCGAATGCAACTTTACTACGTTACACTTCGACTTTTCCTTGGT

V P F A A R A Y V E M M Q C E A E K E P -

TTGGTTAGAGTTTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGTGCTGTTGACAAG
1261 -----+-----+-----+-----+-----+ 1320
AACCAATCTCAAAACCAATTGCTGTCTCAACAAGGTAACGTGCCAACACGACAACCTGTTT

L V R V L V N D R V V P L H G C A V D K -

TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTTCGCTAGATCTGGTGGT
1321 -----+-----+-----+-----+-----+ 1380
AACCCATCTACATTCTCTCTGCTGAAGCAACTTCCAAACAGAAAGCGATCTAGACCACCA

L G R C K R D D F V E G L S F A R S G G -

AACTGGGAAGAATGTTTCGCTTAA
1381 -----+-----+----- 1404
TTGACCCCTTCTTACAAAGCGAATT

N W E E C F A *
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Fig. 25c

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<151> 1999-01-22

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<151> 1999-09-21

<160> 89

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<212> PRT

<213> Aspergillus terreus 9A-1

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Glu	Leu	Ser	His	Lys	Trp	Gly	Leu	Tyr	Ala	Pro	Tyr	Phe	Ser	Leu	Gln
			20					25					30		

Asp	Glu	Ser	Pro	Phe	Pro	Leu	Asp	Val	Pro	Glu	Asp	Cys	His	Ile	Thr
		35					40					45			

Phe	Val	Gln	Val	Leu	Ala	Arg	His	Gly	Ala	Arg	Ser	Pro	Thr	His	Ser
	50					55					60				

Lys	Thr	Lys	Ala	Tyr	Ala	Ala	Thr	Ile	Ala	Ala	Ile	Gln	Lys	Ser	Ala
65					70					75					80

Thr	Ala	Phe	Pro	Gly	Lys	Tyr	Ala	Phe	Leu	Gln	Ser	Tyr	Asn	Tyr	Ser
				85					90					95	

Leu	Asp	Ser	Glu	Glu	Leu	Thr	Pro	Phe	Gly	Arg	Asn	Gln	Leu	Arg	Asp
			100					105					110		

Leu	Gly	Ala	Gln	Phe	Tyr	Glu	Arg	Tyr	Asn	Ala	Leu	Thr	Arg	His	Ile
		115					120					125			

Asn	Pro	Phe	Val	Arg	Ala	Thr	Asp	Ala	Ser	Arg	Val	His	Glu	Ser	Ala
	130					135					140				

2

Glu Lys Phe Val Glu Gly Phe Gln Thr Ala Arg Gln Asp Asp His His
 145 150 155 160
 Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Ala Ile Pro Glu
 165 170 175
 Gly Ser Ala Tyr Asn Asn Thr Leu Glu His Ser Leu Cys Thr Ala Phe
 180 185 190
 Glu Ser Ser Thr Val Gly Asp Asp Ala Val Ala Asn Phe Thr Ala Val
 195 200 205
 Phe Ala Pro Ala Ile Ala Gln Arg Leu Glu Ala Asp Leu Pro Gly Val
 210 215 220
 Gln Leu Ser Thr Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
 225 230 235 240
 Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
 245 250 255
 Asp Leu Phe Thr Ala Thr Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
 260 265 270
 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
 275 280 285
 Gln Gly Val Gly Trp Ala Asn Glu Leu Met Ala Arg Leu Thr Arg Ala
 290 295 300
 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Ser Pro
 305 310 315 320
 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335
 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350
 Ala Pro Leu Ser Gln Thr Ser Val Glu Ser Val Ser Gln Thr Asp Gly
 355 360 365
 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
 370 375 380
 Met Met Gln Cys Arg Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400
 Asn Asp Arg Val Met Pro Leu His Gly Cys Pro Thr Asp Lys Leu Gly
 405 410 415
 Arg Cys Lys Arg Asp Ala Phe Val Ala Gly Leu Ser Phe Ala Gln Ala
 420 425 430

3

Gly Gly Asn Trp Ala Asp Cys Phe
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<212> PRT

<213> *Aspergillus terreus* cbs

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Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
 20 25 30

Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr
 35 40 45

Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser
 50 55 60

Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala
 65 70 75 80

Thr Ala Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser
 85 90 95

Met Gly Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp
 100 105 110

Leu Gly Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile
 115 120 125

Asn Pro Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala
 130 135 140

Glu Lys Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His
 145 150 155 160

Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu
 165 170 175

Gly Thr Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe
 180 185 190

Glu Ala Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val
 195 200 205

Phe Ala Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val
 210 215 220

Gln Leu Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
 225 230 235 240

Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
 245 250 255
 Asp Leu Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
 260 265 270
 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
 275 280 285
 Gln Gly Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
 290 295 300
 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro
 305 310 315 320
 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335
 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350
 Lys Pro Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly
 355 360 365
 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu
 370 375 380
 Met Met Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val
 385 390 395 400
 Asn Asp Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly
 405 410 415
 Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala
 420 425 430
 Gly Gly Asn Trp Ala Glu Cys Phe
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<211> 441

<212> PRT

<213> *Aspergillus niger* var. *awamori*

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 20 25 30

5

Asn Glu Ser Ala Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
 35 40 45
 Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
 50 55 60
 Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
 65 70 75 80
 Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
 85 90 95
 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
 100 105 110
 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
 115 120 125
 Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 130 135 140
 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 145 150 155 160
 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 165 170 175
 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 180 185 190
 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 195 200 205
 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 210 215 220
 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 225 230 235 240
 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 245 250 255
 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Gln Ser
 260 265 270
 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 275 280 285
 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300
 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala	Thr	Phe	Pro	Leu	Asn	Ser	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp
				325					330					335	
Asn	Gly	Ile	Ile	Ser	Ile	Leu	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr
			340					345					350		
Lys	Pro	Leu	Ser	Thr	Thr	Thr	Val	Glu	Asn	Ile	Thr	Gln	Thr	Asp	Gly
		355					360					365			
Phe	Ser	Ser	Ala	Trp	Thr	Val	Pro	Phe	Ala	Ser	Arg	Leu	Tyr	Val	Glu
	370					375					380				
Met	Met	Gln	Cys	Gln	Ala	Glu	Gln	Glu	Pro	Leu	Val	Arg	Val	Leu	Val
385					390					395					400
Asn	Asp	Arg	Val	Val	Pro	Leu	His	Gly	Cys	Pro	Ile	Asp	Ala	Leu	Gly
			405						410					415	
Arg	Cys	Thr	Arg	Asp	Ser	Phe	Val	Arg	Gly	Leu	Ser	Phe	Ala	Arg	Ser
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          20          25          30
Asn Glu Ser Val Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
          35          40          45
Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
          50          55          60
Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
 65          70          75          80
Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
          85          90          95
Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
          100          105          110
Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
          115          120          125

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Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 130 135 140
 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 145 150 155 160
 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 165 170 175
 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 180 185 190
 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 195 200 205
 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 210 215 220
 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 225 230 235 240
 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 245 250 255
 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Arg Ser
 260 265 270
 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 275 280 285
 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300
 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320
 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335
 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350
 Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
 355 360 365
 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
 370 375 380
 Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400
 Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
 405 410 415

Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asp Trp Ala Glu Cys Phe Ala
 435 440

<210> 5

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<212> PRT

<213> Aspergillus niger NRRL3135

<400> 5

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Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
 20 25 30

Asn Glu Ser Val Ile Ser Pro Glu Val Pro Ala Gly Cys Arg Val Thr
 35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser
 50 55 60

Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Ala
 65 70 75 80

Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
 115 120 125

Val Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 130 135 140

Lys Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 195 200 205

9

Phe Val Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 210 215 220
 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 225 230 235 240
 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 245 250 255
 Asp Leu Phe Thr His Asp Glu Trp Ile Asn Tyr Asp Tyr Leu Gln Ser
 260 265 270
 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 275 280 285
 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300
 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Ser Pro
 305 310 315 320
 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335
 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350
 Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
 355 360 365
 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
 370 375 380
 Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400
 Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Val Asp Ala Leu Gly
 405 410 415
 Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
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 Gly Gly Asp Trp Ala Glu Cys Phe Ala
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<212> PRT

<213> Aspergillus fumigatus 13073

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Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
 35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
 65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
 100 105 110

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
 115 120 125

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
 130 135 140

Ala Ser Gln Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly
 145 150 155 160

Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro
 165 170 175

Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys
 180 185 190

Phe Ile Glu Gly Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
 195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
 210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
 245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
 260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320
 Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
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 Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
 340 345 350
 Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365
 Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380
 Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400
 Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415
 Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430
 Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

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<212> PRT

<213> Aspergillus fumigatus 32722

<400> 7

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 20 25 30
 Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
 35 40 45
 Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60
 Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
 65 70 75 80
 Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

12

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
 100 105 110
 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
 115 120 125
 Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140
 Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
 145 150 155 160
 Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175
 Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
 180 185 190
 Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
 195 200 205
 Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
 210 215 220
 Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240
 Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
 245 250 255
 Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
 260 265 270
 Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285
 Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300
 Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320
 Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
 325 330 335
 Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Gly
 340 345 350
 Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365
 Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380

13

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430

Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

<210> 8

<211> 440

<212> PRT

<213> Aspergillus fumigatus 58128

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 20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
 35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
 65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
 115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
 145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
 180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
 195 200 205
 Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
 210 215 220
 Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240
 Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
 245 250 255
 Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
 260 265 270
 Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285
 Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300
 Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320
 Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
 325 330 335
 Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
 340 345 350
 Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365
 Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380
 Met Gln Cys Lys Ser Glu Lys Glu Ser Leu Val Arg Ala Leu Ile Asn
 385 390 395 400
 Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415
 Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
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 Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

<210> 9

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<213> Aspergillus fumigatus 26906

15

<400> 9

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Ala	Thr	Ser	His	Leu	Trp	Gly	Gln	Tyr	Ser	Pro	Phe	Phe	Ser	Leu	Glu	20	25	30	
Asp	Glu	Leu	Ser	Val	Ser	Ser	Lys	Leu	Pro	Lys	Asp	Cys	Arg	Ile	Thr	35	40	45	
Leu	Val	Gln	Val	Leu	Ser	Arg	His	Gly	Ala	Arg	Tyr	Pro	Thr	Ser	Ser	50	55	60	
Lys	Ser	Lys	Lys	Tyr	Lys	Lys	Leu	Val	Thr	Ala	Ile	Gln	Ala	Asn	Ala	65	70	75	80
Thr	Asp	Phe	Lys	Gly	Lys	Phe	Ala	Phe	Leu	Lys	Thr	Tyr	Asn	Tyr	Thr	85	90	95	
Leu	Gly	Ala	Asp	Asp	Leu	Thr	Ala	Phe	Gly	Glu	Gln	Gln	Leu	Val	Asn	100	105	110	
Ser	Gly	Ile	Lys	Phe	Tyr	Gln	Arg	Tyr	Lys	Ala	Leu	Ala	Arg	Ser	Val	115	120	125	
Val	Pro	Phe	Ile	Arg	Ala	Ser	Gly	Ser	Asp	Arg	Val	Ile	Ala	Ser	Gly	130	135	140	
Glu	Lys	Phe	Ile	Glu	Gly	Phe	Gln	Gln	Ala	Lys	Leu	Ala	Asp	Pro	Gly	145	150	155	160
Ala	Thr	Asn	Arg	Ala	Ala	Pro	Ala	Ile	Ser	Val	Ile	Ile	Pro	Glu	Ser	165	170	175	
Glu	Thr	Phe	Asn	Asn	Thr	Leu	Asp	His	Gly	Val	Cys	Thr	Lys	Phe	Glu	180	185	190	
Ala	Ser	Gln	Leu	Gly	Asp	Glu	Val	Ala	Ala	Asn	Phe	Thr	Ala	Leu	Phe	195	200	205	
Ala	Pro	Asp	Ile	Arg	Ala	Arg	Ala	Lys	Lys	His	Leu	Pro	Gly	Val	Thr	210	215	220	
Leu	Thr	Asp	Glu	Asp	Val	Val	Ser	Leu	Met	Asp	Met	Cys	Ser	Phe	Asp	225	230	235	240
Thr	Val	Ala	Arg	Thr	Ser	Asp	Ala	Ser	Gln	Leu	Ser	Pro	Phe	Cys	Gln	245	250	255	
Leu	Phe	Thr	His	Asn	Glu	Trp	Lys	Lys	Tyr	Asn	Tyr	Leu	Gln	Ser	Leu	260	265	270	

Gly	Lys	Tyr	Tyr	Gly	Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln
		275					280					285			
Gly	Ile	Gly	Phe	Thr	Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	Arg	Ser	Pro
		290				295					300				
Val	Gln	Asp	His	Thr	Ser	Thr	Asn	Ser	Thr	Leu	Val	Ser	Asn	Pro	Ala
305					310					315					320
Thr	Phe	Pro	Leu	Asn	Ala	Thr	Met	Tyr	Val	Asp	Phe	Ser	His	Asp	Asn
				325					330					335	
Ser	Met	Val	Ser	Ile	Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Glu
			340					345					350		
Pro	Leu	Ser	Arg	Thr	Ser	Val	Glu	Ser	Ala	Lys	Glu	Leu	Asp	Gly	Tyr
		355					360					365			
Ser	Ala	Ser	Trp	Val	Val	Pro	Phe	Gly	Ala	Arg	Ala	Tyr	Phe	Glu	Thr
	370					375					380				
Met	Gln	Cys	Lys	Ser	Glu	Lys	Glu	Pro	Leu	Val	Arg	Ala	Leu	Ile	Asn
385					390					395					400
Asp	Arg	Val	Val	Pro	Leu	His	Gly	Cys	Asp	Val	Asp	Lys	Leu	Gly	Arg
				405				410						415	
Cys	Lys	Leu	Asn	Asp	Phe	Val	Lys	Gly	Leu	Ser	Trp	Ala	Arg	Ser	Gly
			420					425					430		
Gly	Asn	Trp	Gly	Glu	Cys	Phe	Ser								
		435					440								

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<210> 10
<211> 440
<212> PRT
<213> Aspergillus fumigatus 32239
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<400> 10
Gly Ser Lys Ala Cys Asp Thr Val Glu Leu Gly Tyr Gln Cys Ser Pro
  1          5          10          15
Gly Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
          20          25          30
Asp Glu Leu Ser Val Ser Ser Asp Leu Pro Lys Asp Cys Arg Val Thr
          35          40          45
Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ala Ser
          50          55          60
Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Lys Asn Ala
  65          70          75          80

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Thr Glu Phe Lys Gly Lys Phe Ala Phe Leu Glu Thr Tyr Asn Tyr Thr
 85 90 95
 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
 100 105 110
 Ser Gly Ile Lys Phe Tyr Gln Lys Tyr Lys Ala Leu Ala Gly Ser Val
 115 120 125
 Val Pro Phe Ile Arg Ser Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140
 Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Asn Val Ala Asp Pro Gly
 145 150 155 160
 Ala Thr Asn Arg Ala Ala Pro Val Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175
 Glu Thr Tyr Asn Asn Thr Leu Asp His Ser Val Cys Thr Asn Phe Glu
 180 185 190
 Ala Ser Glu Leu Gly Asp Glu Val Glu Ala Asn Phe Thr Ala Leu Phe
 195 200 205
 Ala Pro Ala Ile Arg Ala Arg Ile Glu Lys His Leu Pro Gly Val Gln
 210 215 220
 Leu Thr Asp Asp Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240
 Thr Val Ala Arg Thr Ala Asp Ala Ser Glu Leu Ser Pro Phe Cys Ala
 245 250 255
 Ile Phe Thr His Asn Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu
 260 265 270
 Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285
 Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Pro
 290 295 300
 Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Asp Ser Asp Pro Ala
 305 310 315 320
 Thr Phe Pro Leu Asn Ala Thr Ile Tyr Val Asp Phe Ser His Asp Asn
 325 330 335
 Gly Met Ile Pro Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Glu
 340 345 350
 Pro Leu Ser Gln Thr Ser Glu Glu Ser Thr Lys Glu Ser Asn Gly Tyr
 355 360 365

Ser Ala Ser Trp Ala Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg
 405 410 415

Cys Lys Leu Lys Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430

Gly Asn Ser Glu Gln Ser Phe Ser
 435 440

<210> 11

<211> 439

<212> PRT

<213> Emericella nidulans

<400> 11

Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys Phe Pro
 1 5 10 15

Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Ile Glu
 20 25 30

Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu Val Thr
 35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
 50 55 60

Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys Asn Ala
 65 70 75 80

Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Ile Phe Gly Glu Asn Gln Met Val Asp
 100 105 110

Ser Gly Ala Lys Phe Tyr Arg Arg Tyr Lys Asn Leu Ala Arg Lys Asn
 115 120 125

Thr Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Val Ala Ser Ala
 130 135 140

Glu Lys Phe Ile Asn Gly Phe Arg Lys Ala Gln Leu His Asp His Gly
 145 150 155 160

19

Ser Gly Gln Ala Thr Pro Val Val Asn Val Ile Ile Pro Glu Ile Asp
 165 170 175
 Gly Phe Asn Asn Thr Leu Asp His Ser Thr Cys Val Ser Phe Glu Asn
 180 185 190
 Asp Glu Arg Ala Asp Glu Ile Glu Ala Asn Phe Thr Ala Ile Met Gly
 195 200 205
 Pro Pro Ile Arg Lys Arg Leu Glu Asn Asp Leu Pro Gly Ile Lys Leu
 210 215 220
 Thr Asn Glu Asn Val Ile Tyr Leu Met Asp Met Cys Ser Phe Asp Thr
 225 230 235 240
 Met Ala Arg Thr Ala His Gly Thr Glu Leu Ser Pro Phe Cys Ala Ile
 245 250 255
 Phe Thr Glu Lys Glu Trp Leu Gln Tyr Asp Tyr Leu Gln Ser Leu Ser
 260 265 270
 Lys Tyr Tyr Gly Tyr Gly Ala Gly Ser Pro Leu Gly Pro Ala Gln Gly
 275 280 285
 Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Gln Ser Pro Val
 290 295 300
 Gln Asp Asn Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr
 305 310 315 320
 Phe Pro Leu Asp Arg Lys Leu Tyr Ala Asp Phe Ser His Asp Asn Ser
 325 330 335
 Met Ile Ser Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Gln Pro
 340 345 350
 Leu Ser Met Asp Ser Val Glu Ser Ile Gln Glu Met Asp Gly Tyr Ala
 355 360 365
 Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Leu Met
 370 375 380
 Gln Cys Glu Lys Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg
 385 390 395 400
 Val Val Pro Leu His Gly Cys Ala Val Asp Lys Phe Gly Arg Cys Thr
 405 410 415
 Leu Asp Asp Trp Val Glu Gly Leu Asn Phe Ala Arg Ser Gly Gly Asn
 420 425 430
 Trp Lys Thr Cys Phe Thr Leu
 435

<210> 12
 <211> 443
 <212> PRT
 <213> Talaromyces thermophilus

<400> 12

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Asp Ser His Ser Cys Asn Thr Val Glu Gly Gly Tyr Gln Cys Arg Pro
 1              5              10              15

Glu Ile Ser His Ser Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
      20              25              30

Asp Gln Ser Glu Ile Ser Pro Asp Val Pro Gln Asn Cys Lys Ile Thr
      35              40              45

Phe Val Gln Leu Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50              55              60

Lys Thr Glu Leu Tyr Ser Gln Leu Ile Ser Arg Ile Gln Lys Thr Ala
 65              70              75              80

Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe Leu Lys Asp Tyr Arg Tyr Gln
      85              90              95

Leu Gly Ala Asn Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Ile Gln
      100              105              110

Leu Gly Ile Lys Phe Tyr Asn His Tyr Lys Ser Leu Ala Arg Asn Ala
      115              120              125

Val Pro Phe Val Arg Cys Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
      130              135              140

Arg Leu Phe Ile Glu Gly Phe Gln Ser Ala Lys Val Leu Asp Pro His
      145              150              155              160

Ser Asp Lys His Asp Ala Pro Pro Thr Ile Asn Val Ile Ile Glu Glu
      165              170              175

Gly Pro Ser Tyr Asn Asn Thr Leu Asp Thr Gly Ser Cys Pro Val Phe
      180              185              190

Glu Asp Ser Ser Gly Gly His Asp Ala Gln Glu Lys Phe Ala Lys Gln
      195              200              205

Phe Ala Pro Ala Ile Leu Glu Lys Ile Lys Asp His Leu Pro Gly Val
      210              215              220

Asp Leu Ala Val Ser Asp Val Pro Tyr Leu Met Asp Leu Cys Pro Phe
      225              230              235              240

Glu Thr Leu Ala Arg Asn His Thr Asp Thr Leu Ser Pro Phe Cys Ala
      245              250              255

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Leu Ser Thr Gln Glu Glu Trp Gln Ala Tyr Asp Tyr Tyr Gln Ser Leu
 260 265 270
 Gly Lys Tyr Tyr Gly Asn Gly Gly Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285
 Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met Thr His Ser Pro
 290 295 300
 Val Gln Asp Tyr Thr Thr Val Asn His Thr Leu Asp Ser Asn Pro Ala
 305 310 315 320
 Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn
 325 330 335
 Thr Met Thr Ser Ile Phe Ala Ala Leu Gly Leu Tyr Asn Gly Thr Ala
 340 345 350
 Lys Leu Ser Thr Thr Glu Ile Lys Ser Ile Glu Glu Thr Asp Gly Tyr
 355 360 365
 Ser Ala Ala Trp Thr Val Pro Phe Gly Gly Arg Ala Tyr Ile Glu Met
 370 375 380
 Met Gln Cys Asp Asp Ser Asp Glu Pro Val Val Arg Val Leu Val Asn
 385 390 395 400
 Asp Arg Val Val Pro Leu His Gly Cys Glu Val Asp Ser Leu Gly Arg
 405 410 415
 Cys Lys Arg Asp Asp Phe Val Arg Gly Leu Ser Phe Ala Arg Gln Gly
 420 425 430
 Gly Asn Trp Glu Gly Cys Tyr Ala Ala Ser Glu
 435 440

<210> 13

<211> 466

<212> PRT

<213> Myceliophthora thermophila

<400> 13

Glu Ser Arg Pro Cys Asp Thr Pro Asp Leu Gly Phe Gln Cys Gly Thr
 1 5 10 15
 Ala Ile Ser His Phe Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Val Pro
 20 25 30
 Ser Glu Leu Asp Ala Ser Ile Pro Asp Asp Cys Glu Val Thr Phe Ala
 35 40 45

22

Gln Val Leu Ser Arg His Gly Ala Arg Ala Pro Thr Leu Lys Arg Ala
 50 55 60
 Ala Ser Tyr Val Asp Leu Ile Asp Arg Ile His His Gly Ala Ile Ser
 65 70 75 80
 Tyr Gly Pro Gly Tyr Glu Phe Leu Arg Thr Tyr Asp Tyr Thr Leu Gly
 85 90 95
 Ala Asp Glu Leu Thr Arg Thr Gly Gln Gln Gln Met Val Asn Ser Gly
 100 105 110
 Ile Lys Phe Tyr Arg Arg Tyr Arg Ala Leu Ala Arg Lys Ser Ile Pro
 115 120 125
 Phe Val Arg Thr Ala Gly Gln Asp Arg Val Val His Ser Ala Glu Asn
 130 135 140
 Phe Thr Gln Gly Phe His Ser Ala Leu Leu Ala Asp Arg Gly Ser Thr
 145 150 155 160
 Val Arg Pro Thr Leu Pro Tyr Asp Met Val Val Ile Pro Glu Thr Ala
 165 170 175
 Gly Ala Asn Asn Thr Leu His Asn Asp Leu Cys Thr Ala Phe Glu Glu
 180 185 190
 Gly Pro Tyr Ser Thr Ile Gly Asp Asp Ala Gln Asp Thr Tyr Leu Ser
 195 200 205
 Thr Phe Ala Gly Pro Ile Thr Ala Arg Val Asn Ala Asn Leu Pro Gly
 210 215 220
 Ala Asn Leu Thr Asp Ala Asp Thr Val Ala Leu Met Asp Leu Cys Pro
 225 230 235 240
 Phe Glu Thr Val Ala Ser Ser Ser Ser Asp Pro Ala Thr Ala Asp Ala
 245 250 255
 Gly Gly Gly Asn Gly Arg Pro Leu Ser Pro Phe Cys Arg Leu Phe Ser
 260 265 270
 Glu Ser Glu Trp Arg Ala Tyr Asp Tyr Leu Gln Ser Val Gly Lys Trp
 275 280 285
 Tyr Gly Tyr Gly Pro Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly
 290 295 300
 Phe Val Asn Glu Leu Leu Ala Arg Leu Ala Gly Val Pro Val Arg Asp
 305 310 315 320
 Gly Thr Ser Thr Asn Arg Thr Leu Asp Gly Asp Pro Arg Thr Phe Pro
 325 330 335

23

Leu Gly Arg Pro Leu Tyr Ala Asp Phe Ser His Asp Asn Asp Met Met
 340 345 350
 Gly Val Leu Gly Ala Leu Gly Ala Tyr Asp Gly Val Pro Pro Leu Asp
 355 360 365
 Lys Thr Ala Arg Arg Asp Pro Glu Glu Leu Gly Gly Tyr Ala Ala Ser
 370 375 380
 Trp Ala Val Pro Phe Ala Ala Arg Ile Tyr Val Glu Lys Met Arg Cys
 385 390 395 400
 Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Gly Arg Gln Glu Lys
 405 410 415
 Asp Glu Glu Met Val Arg Val Leu Val Asn Asp Arg Val Met Thr Leu
 420 425 430
 Lys Gly Cys Gly Ala Asp Glu Arg Gly Met Cys Thr Leu Glu Arg Phe
 435 440 445
 Ile Glu Ser Met Ala Phe Ala Arg Gly Asn Gly Lys Trp Asp Leu Cys
 450 455 460
 Phe Ala
 465

<210> 14

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
 phytase

<400> 14

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
 1 5 10 15
 Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu
 20 25 30
 Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr
 35 40 45
 Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60
 Lys Ser Lys Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
 65 70 75 80

24

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95
 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn
 100 105 110
 Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
 115 120 125
 Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
 130 135 140
 Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
 145 150 155 160
 Ser Gln Pro His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu
 165 170 175
 Gly Ser Gly Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe
 180 185 190
 Glu Asp Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu
 195 200 205
 Phe Ala Pro Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val
 210 215 220
 Thr Leu Thr Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe
 225 230 235 240
 Glu Thr Val Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys
 245 250 255
 Ala Leu Phe Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser
 260 265 270
 Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
 275 280 285
 Gln Gly Val Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
 290 295 300
 Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320
 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335
 Asn Ser Met Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350
 Ala Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
 355 360 365

25

Tyr Ser Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu
 370 375 380

Met Met Gln Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly
 405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe Ala
 435 440

<210> 15

<211> 1426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
 phytase

<220>

<221> CDS

<222> (12)..(1412)

<220>

<221> sig_peptide

<222> (12)..(89)

<220>

<221> mat_peptide

<222> (90)..(1412)

<400> 15

tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg 50
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
 -25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
 Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
 -10 -5 -1 1

tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
 Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
 5 10 15

cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct 194
 His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser
 20 25 30 35

26

gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa	242
Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln	
40 45 50	
ggt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag	290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys	
55 60 65	
gct tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc	338
Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe	
70 75 80	
aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct	386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala	
85 90 95	
gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att	434
Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile	
100 105 110 115	
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc	482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe	
120 125 130	
att aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc	530
Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe	
135 140 145	
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca	578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro	
150 155 160	
cac caa gct tct cca gtt att gac gtt att att cca gaa gga tcc ggt	626
His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly	
165 170 175	
tac aac aac act ttg gac cac ggt act tgt act gct ttc gaa gac tct	674
Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser	
180 185 190 195	
gaa ttg ggt gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca	722
Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro	
200 205 210	
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act	770
Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr	
215 220 225	
gac gaa gac gtt gtt tac ttg atg gac atg tgt cca ttc gaa act gtt	818
Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val	
230 235 240	
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc	866
Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe	

27

245	250	255	
act cac gac gaa tgg aga caa tac gac tac ttg caa tct ttg ggt aag			914
Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys			
260	265	270	275
tac tac ggt tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt			962
Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val			
	280	285	290
ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa			1010
Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln			
	295	300	305
gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc			1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe			
	310	315	320
cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac tct atg			1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met			
	325	330	335
att tct att ttc ttc gct ttg ggt ttg tac aac ggt act gct cca ttg			1154
Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu			
	340	345	350
tct act act tct gtt gaa tct att gaa gaa act gac ggt tac tct gct			1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala			
	360	365	370
tct tgg act gtt cca ttc ggt gct aga gct tac gtt gaa atg atg caa			1250
Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln			
	375	380	385
tgt caa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga			1298
Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg			
	390	395	400
gtt gtt cca ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag			1346
Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys			
	405	410	415
aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac			1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn			
	420	425	430
tggt gct gaa tgt ttc gct taagaattca tata			1426
Trp Ala Glu Cys Phe Ala			
	440		

<210> 16

<211> 467

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: consensus
phytase

<400> 16

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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25                -20                -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10                -5                -1    1                5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
          10                15                20

Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser
          25                30                35

Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
          40                45                50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
          55                60                65                70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
          75                80                85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
          90                95                100

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
          105                110                115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
          120                125                130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
          135                140                145                150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
          155                160                165

Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
          170                175                180

Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
          185                190                195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
          200                205                210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
          215                220                225                230

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29

Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val Ala Arg Thr
 235 240 245
 Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260
 Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275
 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 280 285 290
 Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
 295 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325
 Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met Ile Ser Ile
 330 335 340
 Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr
 345 350 355
 Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370
 Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 375 380 385 390
 Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405
 Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435
 Cys Phe Ala
 440

<210> 17

<211> 422

<212> PRT

<213> Paxillus involutus phyA1

<400> 17

Ser Val Pro Lys Asn Thr Ala Pro Thr Phe Pro Ile Pro Glu Ser Glu
 1 5 10 15

30

Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
 20 25 30
 Lys Ala Pro Pro Ala Gly Cys Gln Ile Asn Gln Val Asn Ile Ile Gln
 35 40 45
 Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Thr Thr Arg Ile Lys
 50 55 60
 Ala Gly Leu Thr Lys Leu Gln Gly Val Gln Asn Phe Thr Asp Ala Lys
 65 70 75 80
 Phe Asn Phe Ile Lys Ser Phe Lys Tyr Asp Leu Gly Asn Ser Asp Leu
 85 90 95
 Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Gln Glu Ala Phe
 100 105 110
 Ala Arg Tyr Ser Lys Leu Val Ser Lys Asn Asn Leu Pro Phe Ile Arg
 115 120 125
 Ala Asp Gly Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala
 130 135 140
 Gly Phe Ala Ser Ala Ser His Asn Thr Val Gln Pro Lys Leu Asn Leu
 145 150 155 160
 Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
 165 170 175
 Ala Ala Gly Asp Ser Asp Pro Gln Val Asn Ala Trp Leu Ala Val Ala
 180 185 190
 Phe Pro Ser Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro Ser Val Asn
 195 200 205
 Leu Thr Asp Thr Asp Ala Phe Asn Leu Val Ser Leu Cys Ala Phe Leu
 210 215 220
 Thr Val Ser Lys Glu Lys Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
 225 230 235 240
 Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Gly Gly Asp Leu Asp Lys
 245 250 255
 Phe Tyr Gly Thr Gly Tyr Gly Gln Glu Leu Gly Pro Val Gln Gly Val
 260 265 270
 Gly Tyr Val Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Ala Val Arg
 275 280 285
 Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ser Pro Val Thr Phe
 290 295 300

31

Pro Leu Asn Lys Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Leu Met
 305 310 315 320
 Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Pro Ala Pro Leu
 325 330 335
 Ser Thr Ser Val Pro Asn Pro Trp Arg Thr Trp Arg Thr Ser Ser Leu
 340 345 350
 Val Pro Phe Ser Gly Arg Met Val Val Glu Arg Leu Ser Cys Phe Gly
 355 360 365
 Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
 370 375 380
 Phe Cys Gly Gly Asp Arg Asn Gly Leu Cys Thr Leu Ala Lys Phe Val
 385 390 395 400
 Glu Ser Gln Thr Phe Ala Arg Ser Asp Gly Ala Gly Asp Phe Glu Lys
 405 410 415
 Cys Phe Ala Thr Ser Ala
 420

<210> 18
 <211> 422
 <212> PRT
 <213> Paxillus involutus phyA2

<400> 18
 Ser Val Pro Arg Asn Ile Ala Pro Lys Phe Ser Ile Pro Glu Ser Glu
 1 5 10 15
 Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
 20 25 30
 Lys Ala Pro Pro Ala Gly Cys Glu Ile Asn Gln Val Asn Ile Ile Gln
 35 40 45
 Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Lys
 50 55 60
 Ala Gly Leu Ser Lys Leu Gln Ser Val Gln Asn Phe Thr Asp Pro Lys
 65 70 75 80
 Phe Asp Phe Ile Lys Ser Phe Thr Tyr Asp Leu Gly Thr Ser Asp Leu
 85 90 95
 Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Leu Glu Val Phe
 100 105 110
 Ala Arg Tyr Ser Lys Leu Val Ser Ser Asp Asn Leu Pro Phe Ile Arg
 115 120 125

Ser Asp Gly Ser Asp Arg Val Val Asp Thr Ala Thr Asn Trp Thr Ala
 130 135 140
 Gly Phe Ala Ser Ala Ser Arg Asn Ala Ile Gln Pro Lys Leu Asp Leu
 145 150 155 160
 Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
 165 170 175
 Ala Ala Gly Glu Ser Asp Pro Gln Val Asp Ala Trp Leu Ala Ser Ala
 180 185 190
 Phe Pro Ser Val Thr Ala Gln Leu Asn Ala Ala Ala Pro Gly Ala Asn
 195 200 205
 Leu Thr Asp Ala Asp Ala Phe Asn Leu Val Ser Leu Cys Pro Phe Met
 210 215 220
 Thr Val Ser Lys Glu Gln Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
 225 230 235 240
 Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Ala Gly Asp Leu Asp Lys
 245 250 255
 Phe Tyr Gly Thr Gly Tyr Gly Gln Ala Leu Gly Pro Val Gln Gly Val
 260 265 270
 Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Asn Ser Ala Val Asn
 275 280 285
 Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ala Pro Asp Thr Phe
 290 295 300
 Pro Leu Asn Lys Thr Met Tyr Ala Asp Phe Ser His Asp Asn Leu Met
 305 310 315 320
 Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Ser Ala Pro Leu
 325 330 335
 Ser Thr Ser Thr Pro Asp Pro Asn Arg Thr Trp Leu Thr Ser Ser Val
 340 345 350
 Val Pro Phe Ser Ala Arg Met Ala Val Glu Arg Leu Ser Cys Ala Gly
 355 360 365
 Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
 370 375 380
 Phe Cys Gly Gly Asp Gln Asp Gly Leu Cys Ala Leu Asp Lys Phe Val
 385 390 395 400
 Glu Ser Gln Ala Tyr Ala Arg Ser Gly Gly Ala Gly Asp Phe Glu Lys
 405 410 415

Cys Leu Ala Thr Thr Val
420

<210> 19

<211> 420

<212> PRT

<213> Trametes pubescens

<400> 19

His	Ile	Pro	Leu	Arg	Asp	Thr	Ser	Ala	Cys	Leu	Asp	Val	Thr	Arg	Asp	1	5	10	15
Val	Gln	Gln	Ser	Trp	Ser	Met	Tyr	Ser	Pro	Tyr	Phe	Pro	Ala	Ala	Thr	20	25	30	
Tyr	Val	Ala	Pro	Pro	Ala	Ser	Cys	Gln	Ile	Asn	Gln	Val	His	Ile	Ile	35	40	45	
Gln	Arg	His	Gly	Ala	Arg	Phe	Pro	Thr	Ser	Gly	Ala	Ala	Lys	Arg	Ile	50	55	60	
Gln	Thr	Ala	Val	Ala	Lys	Leu	Lys	Ala	Ala	Ser	Asn	Tyr	Thr	Asp	Pro	65	70	75	80
Leu	Leu	Ala	Phe	Val	Thr	Asn	Tyr	Thr	Tyr	Ser	Leu	Gly	Gln	Asp	Ser	85	90	95	
Leu	Val	Glu	Leu	Gly	Ala	Thr	Gln	Ser	Ser	Glu	Ala	Gly	Gln	Glu	Ala	100	105	110	
Phe	Thr	Arg	Tyr	Ser	Ser	Leu	Val	Ser	Ala	Asp	Glu	Leu	Pro	Phe	Val	115	120	125	
Arg	Ala	Ser	Gly	Ser	Asp	Arg	Val	Val	Ala	Thr	Ala	Asn	Asn	Trp	Thr	130	135	140	
Ala	Gly	Phe	Ala	Leu	Ala	Ser	Ser	Asn	Ser	Ile	Thr	Pro	Val	Leu	Ser	145	150	155	160
Val	Ile	Ile	Ser	Glu	Ala	Gly	Asn	Asp	Thr	Leu	Asp	Asp	Asn	Met	Cys	165	170	175	
Pro	Ala	Ala	Gly	Asp	Ser	Asp	Pro	Gln	Val	Asn	Gln	Trp	Leu	Ala	Gln	180	185	190	
Phe	Ala	Pro	Pro	Met	Thr	Ala	Arg	Leu	Asn	Ala	Gly	Ala	Pro	Gly	Ala	195	200	205	
Asn	Leu	Thr	Asp	Thr	Asp	Thr	Tyr	Asn	Leu	Leu	Thr	Leu	Cys	Pro	Phe	210	215	220	

34

Glu Thr Val Ala Thr Glu Arg Arg Ser Glu Phe Cys Asp Ile Tyr Glu
 225 230 235 240
 Glu Leu Gln Ala Glu Asp Ala Phe Ala Tyr Asn Ala Asp Leu Asp Lys
 245 250 255
 Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val
 260 265 270
 Gly Tyr Ile Asn Glu Leu Ile Ala Arg Leu Thr Ala Gln Asn Val Ser
 275 280 285
 Asp His Thr Gln Thr Asn Ser Thr Leu Asp Ser Ser Pro Glu Thr Phe
 290 295 300
 Pro Leu Asn Arg Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gln Met
 305 310 315 320
 Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln Ser Ala Pro Leu
 325 330 335
 Asp Pro Thr Thr Pro Asp Pro Ala Arg Thr Phe Leu Val Lys Lys Ile
 340 345 350
 Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Asp Cys Gly Gly
 355 360 365
 Ala Gln Ser Val Arg Leu Leu Val Asn Asp Ala Val Gln Pro Leu Ala
 370 375 380
 Phe Cys Gly Ala Asp Thr Ser Gly Val Cys Thr Leu Asp Ala Phe Val
 385 390 395 400
 Glu Ser Gln Ala Tyr Ala Arg Asn Asp Gly Glu Gly Asp Phe Glu Lys
 405 410 415
 Cys Phe Ala Thr
 420

<210> 20

<211> 435

<212> PRT

<213> Agrocybe pediades

<400> 20

Gly Gly Val Val Gln Ala Thr Phe Val Gln Pro Phe Phe Pro Pro Gln
 1 5 10 15
 Ile Gln Asp Ser Trp Ala Ala Tyr Thr Pro Tyr Tyr Pro Val Gln Ala
 20 25 30
 Tyr Thr Pro Pro Pro Lys Asp Cys Lys Ile Thr Gln Val Asn Ile Ile
 35 40 45

Gln Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Gly Thr Arg Ile
 50 55 60
 Gln Ala Ala Val Lys Lys Leu Gln Ser Ala Lys Thr Tyr Thr Asp Pro
 65 70 75 80
 Arg Leu Asp Phe Leu Thr Asn Tyr Thr Tyr Thr Leu Gly His Asp Asp
 85 90 95
 Leu Val Pro Phe Gly Ala Leu Gln Ser Ser Gln Ala Gly Glu Glu Thr
 100 105 110
 Phe Gln Arg Tyr Ser Phe Leu Val Ser Lys Glu Asn Leu Pro Phe Val
 115 120 125
 Arg Ala Ser Ser Ser Asn Arg Val Val Asp Ser Ala Thr Asn Trp Thr
 130 135 140
 Glu Gly Phe Ser Ala Ala Ser His His Val Leu Asn Pro Ile Leu Phe
 145 150 155 160
 Val Ile Leu Ser Glu Ser Leu Asn Asp Thr Leu Asp Asp Ala Met Cys
 165 170 175
 Pro Asn Ala Gly Ser Ser Asp Pro Gln Thr Gly Ile Trp Thr Ser Ile
 180 185 190
 Tyr Gly Thr Pro Ile Ala Asn Arg Leu Asn Gln Gln Ala Pro Gly Ala
 195 200 205
 Asn Ile Thr Ala Ala Asp Val Ser Asn Leu Ile Pro Leu Cys Ala Phe
 210 215 220
 Glu Thr Ile Val Lys Glu Thr Pro Ser Pro Phe Cys Asn Leu Phe Thr
 225 230 235 240
 Pro Glu Glu Phe Ala Gln Phe Glu Tyr Phe Gly Asp Leu Asp Lys Phe
 245 250 255
 Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val Gly
 260 265 270
 Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Glu Met Pro Val Arg Asp
 275 280 285
 Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser Ser Pro Leu Thr Phe Pro
 290 295 300
 Leu Asp Arg Ser Ile Tyr Ala Asp Leu Ser His Asp Asn Gln Met Ile
 305 310 315 320
 Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln Ser Ser Pro Leu Asp
 325 330 335

Pro Ser Phe Pro Asn Pro Lys Arg Thr Trp Val Thr Ser Arg Leu Thr
 340 345 350
 Pro Phe Ser Ala Arg Met Val Thr Glu Arg Leu Leu Cys Gln Arg Asp
 355 360 365
 Gly Thr Gly Ser Gly Gly Pro Ser Arg Ile Met Arg Asn Gly Asn Val
 370 375 380
 Gln Thr Phe Val Arg Ile Leu Val Asn Asp Ala Leu Gln Pro Leu Lys
 385 390 395 400
 Phe Cys Gly Gly Asp Met Asp Ser Leu Cys Thr Leu Glu Ala Phe Val
 405 410 415
 Glu Ser Gln Lys Tyr Ala Arg Glu Asp Gly Gln Gly Asp Phe Glu Lys
 420 425 430
 Cys Phe Asp
 435

<210> 21
 <211> 419
 <212> PRT
 <213> Peniophora lycii

<400> 21
 Ser Thr Gln Phe Ser Phe Val Ala Ala Gln Leu Pro Ile Pro Ala Gln
 1 5 10 15
 Asn Thr Ser Asn Trp Gly Pro Tyr Asp Pro Phe Phe Pro Val Glu Pro
 20 25 30
 Tyr Ala Ala Pro Pro Glu Gly Cys Thr Val Thr Gln Val Asn Leu Ile
 35 40 45
 Gln Arg His Gly Ala Arg Trp Pro Thr Ser Gly Ala Arg Ser Arg Gln
 50 55 60
 Val Ala Ala Val Ala Lys Ile Gln Met Ala Arg Pro Phe Thr Asp Pro
 65 70 75 80
 Lys Tyr Glu Phe Leu Asn Asp Phe Val Tyr Lys Phe Gly Val Ala Asp
 85 90 95
 Leu Leu Pro Phe Gly Ala Asn Gln Ser His Gln Thr Gly Thr Asp Met
 100 105 110
 Tyr Thr Arg Tyr Ser Thr Leu Phe Glu Gly Gly Asp Val Pro Phe Val
 115 120 125

37

Arg Ala Ala Gly Asp Gln Arg Val Val Asp Ser Ser Thr Asn Trp Thr
 130 135 140
 Ala Gly Phe Gly Asp Ala Ser Gly Glu Thr Val Leu Pro Thr Leu Gln
 145 150 155 160
 Val Val Leu Gln Glu Glu Gly Asn Cys Thr Leu Cys Asn Asn Met Cys
 165 170 175
 Pro Asn Glu Val Asp Gly Asp Glu Ser Thr Thr Trp Leu Gly Val Phe
 180 185 190
 Ala Pro Asn Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro Ser Ala Asn
 195 200 205
 Leu Ser Asp Ser Asp Ala Leu Thr Leu Met Asp Met Cys Pro Phe Asp
 210 215 220
 Thr Leu Ser Ser Gly Asn Ala Ser Pro Phe Cys Asp Leu Phe Thr Ala
 225 230 235 240
 Glu Glu Tyr Val Ser Tyr Glu Tyr Tyr Tyr Asp Leu Asp Lys Tyr Tyr
 245 250 255
 Gly Thr Gly Pro Gly Asn Ala Leu Gly Pro Val Gln Gly Val Gly Tyr
 260 265 270
 Val Asn Glu Leu Leu Ala Arg Leu Thr Gly Gln Ala Val Arg Asp Glu
 275 280 285
 Thr Gln Thr Asn Arg Thr Leu Asp Ser Asp Pro Ala Thr Phe Pro Leu
 290 295 300
 Asn Arg Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Pro
 305 310 315 320
 Ile Phe Ala Ala Leu Gly Leu Phe Asn Ala Thr Ala Leu Asp Pro Leu
 325 330 335
 Lys Pro Asp Glu Asn Arg Leu Trp Val Asp Ser Lys Leu Val Pro Phe
 340 345 350
 Ser Gly His Met Thr Val Glu Lys Leu Ala Cys Ser Gly Lys Glu Ala
 355 360 365
 Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe Cys Gly
 370 375 380
 Gly Val Asp Gly Val Cys Glu Leu Ser Ala Phe Val Glu Ser Gln Thr
 385 390 395 400
 Tyr Ala Arg Glu Asn Gly Gln Gly Asp Phe Ala Lys Cys Gly Phe Val
 405 410 415

Pro Ser Glu

<210> 22

<211> 369

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:basidio
consensus

<400> 22

Ser Pro Arg Thr Ala Ala Gln Leu Pro Ile Pro Gln Gln Trp Ser Pro
1 5 10 15Tyr Ser Pro Tyr Phe Pro Val Ala Tyr Ala Pro Pro Ala Gly Cys Gln
20 25 30Ile Gln Val Asn Ile Ile Gln Arg His Gly Ala Arg Phe Pro Thr Ser
35 40 45Gly Ala Ala Thr Arg Ile Gln Ala Ala Val Ala Lys Leu Gln Ser Ala
50 55 60Thr Asp Pro Lys Leu Asp Phe Leu Asn Thr Tyr Leu Gly Asp Asp Leu
65 70 75 80Val Pro Phe Gly Ala Gln Ser Ser Gln Ala Gly Gln Glu Ala Phe Thr
85 90 95Arg Tyr Ser Leu Val Ser Asp Asn Leu Pro Phe Val Arg Ala Ser Gly
100 105 110Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala Gly Phe Ala
115 120 125Ala Ser Asn Thr Pro Leu Val Ile Leu Ser Glu Gly Asn Asp Thr Leu
130 135 140Asp Asp Asn Met Cys Pro Ala Gly Asp Ser Asp Pro Gln Asn Trp Leu
145 150 155 160Ala Val Phe Ala Pro Pro Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro
165 170 175Gly Ala Asn Leu Thr Asp Asp Ala Asn Leu Leu Cys Pro Phe Glu Thr
180 185 190Val Ser Glu Ser Phe Cys Asp Leu Phe Glu Pro Glu Glu Phe Ala Phe
195 200 205

39

Tyr Gly Asp Leu Asp Lys Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu
 210 215 220
 Gly Pro Val Gln Gly Val Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu
 225 230 235 240
 Thr Gln Ala Val Arg Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser
 245 250 255
 Ser Pro Thr Phe Pro Leu Asn Arg Thr Phe Tyr Ala Asp Phe Ser His
 260 265 270
 Asp Asn Gln Met Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln
 275 280 285
 Ser Ala Pro Leu Asp Pro Ser Pro Asp Pro Asn Arg Thr Trp Val Thr
 290 295 300
 Ser Lys Leu Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Cys
 305 310 315 320
 Gly Thr Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe
 325 330 335
 Cys Gly Gly Asp Asp Gly Cys Thr Leu Asp Ala Phe Val Glu Ser Gln
 340 345 350
 Tyr Ala Arg Glu Asp Gly Gln Gly Asp Phe Glu Lys Cys Phe Ala Thr
 355 360 365

Pro

<210> 23
 <211> 440
 <212> PRT
 <213> Thermomyces lanuginosus

<400> 23

Asn Val Asp Ile Ala Arg His Trp Gly Gln Tyr Ser Pro Phe Phe Ser
 1 5 10 15
 Leu Ala Glu Val Ser Glu Ile Ser Pro Ala Val Pro Lys Gly Cys Arg
 20 25 30
 Val Glu Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr
 35 40 45
 Ala His Lys Ser Glu Val Tyr Ala Glu Leu Leu Gln Arg Ile Gln Asp
 50 55 60
 Thr Ala Thr Glu Phe Lys Gly Asp Phe Ala Phe Leu Arg Asp Tyr Ala
 65 70 75 80

Tyr	His	Leu	Gly	Ala	Asp	Asn	Leu	Thr	Arg	Phe	Gly	Glu	Glu	Gln	Met
				85					90					95	
Met	Glu	Ser	Gly	Arg	Gln	Phe	Tyr	His	Arg	Tyr	Arg	Glu	Gln	Ala	Arg
			100					105					110		
Glu	Ile	Val	Pro	Phe	Val	Arg	Ala	Ala	Gly	Ser	Ala	Arg	Val	Ile	Ala
		115					120					125			
Ser	Ala	Glu	Phe	Phe	Asn	Arg	Gly	Phe	Gln	Asp	Ala	Lys	Asp	Arg	Asp
	130					135					140				
Pro	Arg	Ser	Asn	Lys	Asp	Gln	Ala	Glu	Pro	Val	Ile	Asn	Val	Ile	Ile
145					150					155					160
Ser	Glu	Glu	Thr	Gly	Ser	Asn	Asn	Thr	Leu	Asp	Gly	Leu	Thr	Cys	Pro
				165					170					175	
Ala	Ala	Glu	Glu	Ala	Pro	Asp	Pro	Thr	Gln	Pro	Ala	Glu	Phe	Leu	Gln
			180					185					190		
Val	Phe	Gly	Pro	Arg	Val	Leu	Lys	Lys	Ile	Thr	Lys	His	Met	Pro	Gly
	195						200					205			
Val	Asn	Leu	Thr	Leu	Glu	Asp	Val	Pro	Leu	Phe	Met	Asp	Leu	Cys	Pro
	210					215					220				
Phe	Asp	Thr	Val	Gly	Ser	Asp	Pro	Val	Leu	Phe	Pro	Arg	Gln	Leu	Ser
225					230					235					240
Pro	Phe	Cys	His	Leu	Phe	Thr	Ala	Asp	Asp	Trp	Met	Ala	Tyr	Asp	Tyr
				245					250					255	
Tyr	Tyr	Thr	Leu	Asp	Lys	Tyr	Tyr	Ser	His	Gly	Gly	Gly	Ser	Ala	Phe
			260					265					270		
Gly	Pro	Ser	Arg	Gly	Val	Gly	Phe	Val	Asn	Glu	Leu	Ile	Ala	Arg	Met
		275					280					285			
Thr	Gly	Asn	Leu	Pro	Val	Lys	Asp	His	Thr	Thr	Val	Asn	His	Thr	Leu
	290					295					300				
Asp	Asp	Asn	Pro	Glu	Thr	Phe	Pro	Leu	Asp	Ala	Val	Leu	Tyr	Ala	Asp
305					310					315					320
Phe	Ser	His	Asp	Asn	Thr	Met	Thr	Gly	Ile	Phe	Ser	Ala	Met	Gly	Leu
				325					330					335	
Tyr	Asn	Gly	Thr	Lys	Pro	Leu	Ser	Thr	Ser	Lys	Ile	Gln	Pro	Pro	Thr
			340					345					350		
Gly	Ala	Ala	Ala	Asp	Gly	Tyr	Ala	Ala	Ser	Trp	Thr	Val	Pro	Phe	Ala
		355					360					365			

41

Ala Arg Ala Tyr Val Glu Leu Leu Arg Cys Glu Thr Glu Thr Ser Ser
 370 375 380

Glu Glu Glu Glu Glu Gly Glu Asp Glu Pro Phe Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Arg Val Asp Arg Trp Gly
 405 410 415

Arg Cys Arg Arg Asp Glu Trp Ile Lys Gly Leu Thr Phe Ala Arg Gln
 420 425 430

Gly Gly His Trp Asp Arg Cys Phe
 435 440

<210> 24

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus 10

<400> 24

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
 1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
 20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr
 35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Ser Lys Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
 65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
 115 120 125

Val Pro Phe Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
 130 135 140

42

Glu	Lys	Phe	Ile	Glu	Gly	Phe	Gln	Ser	Ala	Lys	Leu	Ala	Asp	Pro	Gly	145	150	155	160
Ala	Asn	Pro	His	Gln	Ala	Ser	Pro	Val	Ile	Asn	Val	Ile	Ile	Pro	Glu	165	170	175	
Gly	Ala	Gly	Tyr	Asn	Asn	Thr	Leu	Asp	His	Gly	Leu	Cys	Thr	Ala	Phe	180	185	190	
Glu	Glu	Ser	Glu	Leu	Gly	Asp	Asp	Val	Glu	Ala	Asn	Phe	Thr	Ala	Val	195	200	205	
Phe	Ala	Pro	Pro	Ile	Arg	Ala	Arg	Leu	Glu	Ala	His	Leu	Pro	Gly	Val	210	215	220	
Asn	Leu	Thr	Asp	Glu	Asp	Val	Val	Asn	Leu	Met	Asp	Met	Cys	Pro	Phe	225	230	235	240
Asp	Thr	Val	Ala	Arg	Thr	Ser	Asp	Ala	Thr	Gln	Leu	Ser	Pro	Phe	Cys	245	250	255	
Asp	Leu	Phe	Thr	His	Asp	Glu	Trp	Ile	Gln	Tyr	Asp	Tyr	Leu	Gln	Ser	260	265	270	
Leu	Gly	Lys	Tyr	Tyr	Gly	Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	275	280	285	
Gln	Gly	Val	Gly	Phe	Val	Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	290	295	300	
Pro	Val	Gln	Asp	His	Thr	Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	305	310	315	320
Ala	Thr	Phe	Pro	Leu	Asn	Ala	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	325	330	335	
Asn	Thr	Met	Val	Ser	Ile	Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	340	345	350	
Lys	Pro	Leu	Ser	Thr	Thr	Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	355	360	365	
Tyr	Ala	Ala	Ser	Trp	Thr	Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	370	375	380	
Met	Met	Gln	Cys	Glu	Ala	Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	385	390	395	400
Asn	Asp	Arg	Val	Val	Pro	Leu	His	Gly	Cys	Gly	Val	Asp	Lys	Leu	Gly	405	410	415	
Arg	Cys	Lys	Arg	Asp	Asp	Phe	Val	Glu	Gly	Leu	Ser	Phe	Ala	Arg	Ser	420	425	430	

43

Gly Gly Asn Trp Glu Glu Cys Phe Ala
 435 440

<210> 25

<211> 1426

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
 phytase 10

<220>

<221> CDS

<222> (12)..(1412)

<220>

<221> mat_peptide

<222> (90)..(1412)

<220>

<221> sig_peptide

<222> (12)..(89)

<400> 25

tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg	50
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu	
-25 -20 -15	
ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac	98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His	
-10 -5 -1 1	
tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct	146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser	
5 10 15	
cac ttg tgg ggt caa tac tct cca ttc ttc tct ttg gct gac gaa tct	194
His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser	
20 25 30 35	
gct att tct cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa	242
Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln	
40 45 50	
gtt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag	290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys	
55 60 65	
aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc	338
Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe	
70 75 80	

44

aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct	386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala	
85 90 95	
gac gac ttg act cca ttc ggt gaa caa caa atg gtt aac tct ggt att	434
Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile	
100 105 110 115	
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc	482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe	
120 125 130	
gtt aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc	530
Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe	
135 140 145	
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt gct aac cca	578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro	
150 155 160	
cac caa gct tct cca gtt att aac gtt att att cca gaa ggt gct ggt	626
His Gln Ala Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly	
165 170 175	
tac aac aac act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct	674
Tyr Asn Asn Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser	
180 185 190 195	
gaa ttg ggt gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca	722
Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro	
200 205 210	
cct att aga gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act	770
Pro Ile Arg Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr	
215 220 225	
gac gaa gac gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt	818
Asp Glu Asp Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val	
230 235 240	
gct aga act tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc	866
Ala Arg Thr Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe	
245 250 255	
act cac gac gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag	914
Thr His Asp Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys	
260 265 270 275	
tac tac ggt tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt	962
Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val	
280 285 290	

45

ggt ttc gtt aac gaa ttg att gct aga ttg act cac tct cca gtt caa 1010
 Gly Phe Val Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln
 295 300 305
 gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc 1058
 Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe
 310 315 320
 cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac act atg 1106
 Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met
 325 330 335
 gtt tct att ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg 1154
 Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu
 340 345 350 355
 tct act act tct gtt gaa tct att gaa gaa act gac ggt tac gct gct 1202
 Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ala Ala
 360 365 370
 tct tgg act gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa 1250
 Ser Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln
 375 380 385
 tgt gaa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga 1298
 Cys Glu Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg
 390 395 400
 gtt gtt cca ttg cac ggt tgt ggt gtt gac aag ttg ggt aga tgt aag 1346
 Val Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys
 405 410 415
 aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac 1394
 Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn
 420 425 430 435
 tgg gaa gaa tgt ttc gct taagaattca tata 1426
 Trp Glu Glu Cys Phe Ala
 440

<210> 26

<211> 467

<212> PRT

<213> Artificial Sequence

 <223> Description of Artificial Sequence: consensus
 phytase 10

<400> 26

 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20
 Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 25 30 35
 Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Ser
 55 60 65 70
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100
 Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Val Arg Ala
 120 125 130
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 155 160 165
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 170 175 180
 Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
 185 190 195
 Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 200 205 210
 Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 215 220 225 230
 Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245
 Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 250 255 260
 Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275
 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
 280 285 290

47

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 295 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325
 Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
 330 335 340
 Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355
 Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr
 360 365 370
 Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
 375 380 385 390
 Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405
 Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
 425 430 435
 Cys Phe Ala
 440

<210> 27
 <211> 437
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 phytase 11

<400> 27
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 1 5 10 15
 Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu
 20 25 30
 Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val
 35 40 45
 Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser
 50 55 60

Lys Lys Tyr Ser Ala Leu Ile Glu Arg Ile Gln Lys Asn Ala Thr Phe
 65 70 75 80
 Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
 85 90 95
 Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile
 100 105 110
 Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Asn Ile Val Pro Phe
 115 120 125
 Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
 130 135 140
 Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Ala His Gln Ala
 145 150 155 160
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
 165 170 175
 Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
 180 185 190
 Asp Asp Ala Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 195 200 205
 Ala Arg Leu Glu Ala Leu Pro Gly Val Asn Leu Thr Asp Glu Asp Val
 210 215 220
 Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr Ser
 225 230 235 240
 Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr Ala Asp Glu
 245 250 255
 Trp Gln Tyr Asp Tyr Leu Gln Ser Leu Lys Tyr Tyr Gly Tyr Gly Ala
 260 265 270
 Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Asn Glu Leu Ile
 275 280 285
 Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr Ser Thr Asn His
 290 295 300
 Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr
 305 310 315 320
 Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile Phe Phe Ala Leu
 325 330 335
 Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Ser Val Glu Ser
 340 345 350

Ile Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala Ala
 355 360 365

Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala Gly Gly Gly Gly Gly
 370 375 380

Glu Gly Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val
 385 390 395 400

Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Leu
 405 410 415

Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp
 420 425 430

Ala Glu Cys Phe Ala
 435

<210> 28

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
 phytase 1 thermo 8 q50t, k91a

<220>

<221> CDS

<222> (1)..(1401)

<220>

<221> mat_peptide

<222> (79)..(1401)

<220>

<221> sig_peptide

<222> (1)..(78)

<400> 28

atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc 48
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -10 -5 -1 1 5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20

50

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct	192
Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser	
25 30 35	
cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa gtt ttg tct	240
Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser	
40 45 50	
aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct	288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser	
55 60 65 70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag	336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75 80 85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100	
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
105 110 115	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
120 125 130	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
135 140 145 150	
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn	
170 175 180	
act ttg gac cac ggt act tgt act gct ttc gaa gac tct gaa tta ggt	672
Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly	
185 190 195	
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg	
200 205 210	
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac	768
Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp	
215 220 225 230	

51

gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act	816
Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac	864
Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp	
250 255 260	
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt	912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	
265 270 275	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct	960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala	
280 285 290	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act	1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr	
295 300 305 310	
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac	1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn	
315 320 325	
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att	1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile	
330 335 340	
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act	1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr	
345 350 355	
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act	1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr	
360 365 370	
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct	1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala	
375 380 385 390	
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca	1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro	
395 400 405	
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac	1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp	
410 415 420	
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gct gaa	1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu	
425 430 435	

tgt ttc gct taa
Cys Phe Ala
440

1404

<210> 29
<211> 467
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: consensus
phytase 1 thermo 8 q50t, k91a

<400> 29
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20
Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25 30 35
Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
55 60 65 70
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180
Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 200 205 210
 Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
 215 220 225 230
 Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245
 Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260
 Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275
 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 280 285 290
 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 295 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325
 Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
 330 335 340
 Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355
 Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370
 Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 375 380 385 390
 Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405
 Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435
 Cys Phe Ala
 440

<210> 30

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: consensus
phytase 10 thermo 3 q50t, k91a

<220>

<221> CDS

<222> (1)..(1401)

<220>

<221> mat_peptide

<222> (79)..(1401)

<220>

<221> sig_peptide

<222> (1)..(78)

<400> 30

atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc	48
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser	
-25 -20 -15	
aca tcc ggt acc gcc ttg ggt cct cgt ggt aac tct cac tct tgt gac	96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp	
-10 -5 -1 1 5	
act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg	144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp	
10 15 20	
ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct	192
Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser	
25 30 35	
cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa gtt ttg tct	240
Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser	
40 45 50	
aga cac ggt gct aga tac cca act tct tct gcg tct aag gcg tac tct	288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser	
55 60 65 70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag	336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75 80 85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100	
act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
105 110 115	

aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
120 125 130	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
135 140 145 150	
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn	
170 175 180	
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct gaa ttg ggt	672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly	
185 190 195	
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg	
200 205 210	
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac	768
Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp	
215 220 225 230	
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act	816
Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac	864
Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp	
250 255 260	
gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag tac tac ggt	912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	
265 270 275	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt	960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val	
280 285 290	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act	1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr	
295 300 305 310	
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac	1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn	
315 320 325	

56

[illegible]

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<210> 31
<211> 467
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: consensus
        phytase 10 thermo 3 α50t, k91a
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<400> 31
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
  -25                -20                -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10                -5                -1      1                5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
      10                15                20

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
      25                30                35

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57

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
 55 60 65 70
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100
 Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 120 125 130
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 155 160 165
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 170 175 180
 Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
 185 190 195
 Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 200 205 210
 Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 215 220 225 230
 Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245
 Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 250 255 260
 Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275
 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
 280 285 290
 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 295 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

58

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
 330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
 375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
 425 430 435

Cys Phe Ala
 440

<210> 32
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Aspergillus
 fumigatus alpha-mutant

<220>
 <221> CDS
 <222> (1)..(1401)

<220>
 <221> mat_peptide
 <222> (79)..(1401)

<220>
 <221> sig_peptide
 <222> (1)..(78)

<400> 32
 atg ggg gtt ttc gtc gtt cta tta tct atc gcg act ctg ttc ggc agc 48
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

59

aca tcg ggc act gcg ctg ggc ccc cgt gga aat cac tcc aag tcc tgc	96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Lys Ser Cys	
-10 -5 -1 1 5	
gat acg gta gac cta ggg tac cag tgc tcc cct gcg act tct cat cta	144
Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu	
10 15 20	
tgg ggc acg tac tcg cca tac ttt tcg ctc gag gac gag ctg tcc gtg	192
Trp Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Leu Ser Val	
25 30 35	
tcg agt aag ctt ccc aag gat tgc cgg atc acc ttg gta cag gtg cta	240
Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu	
40 45 50	
tcg cgc cat gga gcg cgg tac cca acc agc tcc aag agc aaa aag tat	288
Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr	
55 60 65 70	
aag aag ctt att acg gcg atc cag gcc aat gcc acc gac ttc aag ggc	336
Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly	
75 80 85	
aag tac gcc ttt ttg aag acg tac aac tat act ctg ggt gcg gat gac	384
Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp	
90 95 100	
ctc act ccc ttt ggg gag cag cag ctg gtg aac tcg ggc atc aag ttc	432
Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe	
105 110 115	
tac cag agg tac aag gct ctg gcg cgc agt gtg gtg ccg ttt att cgc	480
Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg	
120 125 130	
gcc tca ggc tcg gac cgg gtt att gct tcg gga gag aag ttc atc gag	528
Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu	
135 140 145 150	
ggg ttc cag cag gcg aag ctg gct gat cct ggc gcg acg aac cgc gcc	576
Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala	
155 160 165	
gct ccg gcg att agt gtg att att ccg gag agc gag acg ttc aac aat	624
Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn	
170 175 180	
acg ctg gac cac ggt gtg tgc acg aag ttt gag gcg agt cag ctg gga	672
Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly	
185 190 195	

60

gat gag gtt gcg gcc aat ttc act gcg ctc ttt gca ccc gac atc cga	720
Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg	
200 205 210	
gct cgc ctc gag aag cat ctt cct ggc gtg acg ctg aca gac gag gac	768
Ala Arg Leu Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp	
215 220 225 230	
gtt gtc agt cta atg gac atg tgt ccg ttt gat acg gta gcg cgc acc	816
Val Val Ser Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
agc gac gca agt cag ctg tca ccg ttc tgt caa ctc ttc act cac aat	864
Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn	
250 255 260	
gag tgg aag aag tac gac tac ctt cag tcc ttg ggc aag tac tac ggc	912
Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	
265 270 275	
tac ggc gca ggc aac cct ctg gga ccg gct cag ggg ata ggg ttc acc	960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr	
280 285 290	
aac gag ctg att gcc cgg ttg acg cgt tcg cca gtg cag gac cac acc	1008
Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr	
295 300 305 310	
agc act aac tcg act cta gtc tcc aac ccg gcc acc ttc ccg ttg aac	1056
Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn	
315 320 325	
gct acc atg tac gtc gac ttt tca cac gac aac agc atg gtt tcc atc	1104
Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile	
330 335 340	
ttc ttt gca ttg ggc ctg tac aac ggc act gaa ccc ttg tcc cgg acc	1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr	
345 350 355	
tcg gtg gaa agc gcc aag gaa ttg gat ggg tat tct gca tcc tgg gtg	1200
Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val	
360 365 370	
gtg cct ttc ggc gcg cga gcc tac ttc gag acg atg caa tgc aag tcg	1248
Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser	
375 380 385 390	
gaa aag gag cct ctt gtt cgc gct ttg att aat gac cgg gtt gtg cca	1296
Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro	
395 400 405	

61

ctg cat ggc tgc gat gtg gac aag ctg ggg cga tgc aag ctg aat gac 1344
Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp
410 415 420

ttt gtc aag gga ttg agt tgg gcc aga tct ggg ggc aac tgg gga gag 1392
Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu
425 430 435

tgc ttt agt tga 1404
Cys Phe Ser
440

<210> 33

<211> 467

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: *Aspergillus fumigatus* alpha-mutant

<400> 33

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Lys Ser Cys
-10 -5 -1 1 5

Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu
10 15 20

Trp Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Leu Ser Val
25 30 35

Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu
40 45 50

Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr
55 60 65 70

Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly
75 80 85

Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp
90 95 100

Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe
105 110 115

Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg
120 125 130

Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu
135 140 145 150

Gly	Phe	Gln	Gln	Ala	Lys	Leu	Ala	Asp	Pro	Gly	Ala	Thr	Asn	Arg	Ala	
				155					160					165		
Ala	Pro	Ala	Ile	Ser	Val	Ile	Ile	Pro	Glu	Ser	Glu	Thr	Phe	Asn	Asn	
				170					175					180		
Thr	Leu	Asp	His	Gly	Val	Cys	Thr	Lys	Phe	Glu	Ala	Ser	Gln	Leu	Gly	
				185					190					195		
Asp	Glu	Val	Ala	Ala	Asn	Phe	Thr	Ala	Leu	Phe	Ala	Pro	Asp	Ile	Arg	
				200					205					210		
Ala	Arg	Leu	Glu	Lys	His	Leu	Pro	Gly	Val	Thr	Leu	Thr	Asp	Glu	Asp	
				215					220					225		
Val	Val	Ser	Leu	Met	Asp	Met	Cys	Pro	Phe	Asp	Thr	Val	Ala	Arg	Thr	
				235					240					245		
Ser	Asp	Ala	Ser	Gln	Leu	Ser	Pro	Phe	Cys	Gln	Leu	Phe	Thr	His	Asn	
				250					255					260		
Glu	Trp	Lys	Lys	Tyr	Asp	Tyr	Leu	Gln	Ser	Leu	Gly	Lys	Tyr	Tyr	Gly	
				265					270					275		
Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Ile	Gly	Phe	Thr	
				280					285					290		
Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	Arg	Ser	Pro	Val	Gln	Asp	His	Thr	
				295					300					305		
Ser	Thr	Asn	Ser	Thr	Leu	Val	Ser	Asn	Pro	Ala	Thr	Phe	Pro	Leu	Asn	
				315					320					325		
Ala	Thr	Met	Tyr	Val	Asp	Phe	Ser	His	Asp	Asn	Ser	Met	Val	Ser	Ile	
				330					335					340		
Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Glu	Pro	Leu	Ser	Arg	Thr	
				345					350					355		
Ser	Val	Glu	Ser	Ala	Lys	Glu	Leu	Asp	Gly	Tyr	Ser	Ala	Ser	Trp	Val	
				360					365					370		
Val	Pro	Phe	Gly	Ala	Arg	Ala	Tyr	Phe	Glu	Thr	Met	Gln	Cys	Lys	Ser	
				375					380					385		
Glu	Lys	Glu	Pro	Leu	Val	Arg	Ala	Leu	Ile	Asn	Asp	Arg	Val	Val	Pro	
				395					400					405		
Leu	His	Gly	Cys	Asp	Val	Asp	Lys	Leu	Gly	Arg	Cys	Lys	Leu	Asn	Asp	
				410					415					420		
Phe	Val	Lys	Gly	Leu	Ser	Trp	Ala	Arg	Ser	Gly	Gly	Asn	Trp	Gly	Glu	
				425					430					435		

Cys Phe Ser
440

<210> 34
<211> 1426
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: consensus
phytase 7

<220>
<221> CDS
<222> (12)..(1412)

<220>
<221> mat_peptide
<222> (90)..(1412)

<220>
<221> sig_peptide
<222> (12)..(89)

<400> 34
tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg 50
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
-25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
-10 -5 -1 1

tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
5 10 15

cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct 194
His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser
20 25 30 35

gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa 242
Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln
40 45 50

gtt ttg tct aga cac ggt gct aga tac cca act gac tct aag ggt aag 290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys
55 60 65

aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc 338
Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe
70 75 80

aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct	386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala	
85 90 95	
gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att	434
Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile	
100 105 110 115	
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc	482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe	
120 125 130	
att aga gct tct ggt tct tct aga gtt att gct tct gct gaa aag ttc	530
Ile Arg Ala Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe	
135 140 145	
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca	578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro	
150 155 160	
cac caa gct tct cca gtt att gac gtt att att tct gac gct tct tct	626
His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser	
165 170 175	
tac aac aac act ttg gac cca ggt act tgt act gct ttc gaa gac tct	674
Tyr Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser	
180 185 190 195	
gaa ttg gct gac act gtt gaa gct aac ttc act gct ttg ttc gct cca	722
Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro	
200 205 210	
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act	770
Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr	
215 220 225	
gac act gaa gtt act tac ttg atg gac atg tgt tct ttc gaa act gtt	818
Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val	
230 235 240	
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc	866
Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe	
245 250 255	
act cac gac gaa tgg aga cac tac gac tac ttg caa tct ttg aag aag	914
Thr His Asp Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys	
260 265 270 275	
tac tac ggt cac ggt gct ggt aac cca ttg ggt cca act caa ggt gtt	962
Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val	
280 285 290	

65

ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa 1010
Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln
295 300 305

gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc 1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe
310 315 320

cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac ggt att 1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile
325 330 335

att tct att ttc ttc gct ttg ggt ttg tac aac ggt act gct cca ttg 1154
Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu
340 345 350 355

tct act act tct gtt gaa tct att gaa gaa act gac ggt tac tct tct 1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ser
360 365 370

gct tgg act gtt cca ttc gct tct aga gct tac gtt gaa atg atg caa 1250
Ala Trp Thr Val Pro Phe Ala Ser Arg Ala Tyr Val Glu Met Met Gln
375 380 385

tgt caa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga 1298
 Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg
 390 395 400

gtt gtt cca ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag 1346
Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys
405 410 415

aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac 1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn
420 425 430 435

tgg gct gaa tgt ttc gct taagaattca tata 1426
Trp Ala Glu Cys Phe Ala
440

<210> 35

<211> 467

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: consensus
phytase 7

<400> 35

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20
 Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser
 25 30 35
 Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50
 Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser
 55 60 65 70
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100
 Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 120 125 130
 Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165
 Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser Tyr Asn Asn
 170 175 180
 Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Ala
 185 190 195
 Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 200 205 210
 Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Thr Glu
 215 220 225 230
 Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val Ala Arg Thr
 235 240 245
 Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260
 Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly
 265 270 275
 His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Phe Ala
 280 285 290

67

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
 295 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325
 Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile
 330 335 340
 Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr
 345 350 355
 Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ser Ala Trp Thr
 360 365 370
 Val Pro Phe Ala Ser Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 375 380 385 390
 Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405
 Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435
 Cys Phe Ala
 440

<210> 36
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: consensus
 phytase 12

<400> 36
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 1 5 10 15
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 20 25 30
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser Ser Asn Trp
 35 40 45
 Ser Pro Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 50 55 60

68

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Gln
 65 70 75 80
 Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Ser
 85 90 95
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 100 105 110
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 115 120 125
 Val Pro Phe Gly Ala Asn Gln Ser Ser Gln Ala Gly Ile Lys Phe Tyr
 130 135 140
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 145 150 155 160
 Ser Gly Ser Asp Arg Val Ile Asp Ser Ala Thr Asn Trp Ile Glu Gly
 165 170 175
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 180 185 190
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 195 200 205
 Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
 210 215 220
 Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 225 230 235 240
 Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 245 250 255
 Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 260 265 270
 Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 275 280 285
 Glu Trp Ile Gln Tyr Asp Tyr Leu Gly Asp Leu Asp Lys Tyr Tyr Gly
 290 295 300
 Thr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
 305 310 315 320
 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 325 330 335
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 340 345 350

69

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ala Ile
 355 360 365

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 370 375 380

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Leu
 385 390 395 400

Val Pro Phe Ser Ala Arg Met Tyr Val Glu Met Met Gln Cys Glu Ala
 405 410 415

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 420 425 430

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 435 440 445

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
 450 455 460

Cys Phe Ala
 465

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 37
 tatatgaatt catgggcgtg ttcgtc

26

<210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 38
 tgaaaagttc attgaaggtt tc

22

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
tcttcgaaag cagtacacaa ac 22

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 40
tatatgaatt cttaagcgaa ac 22

<210> 41
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
cacttggtggg gtacctactc tccatacttc tc 32

<210> 42
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
ggtcaataact ctccattctt ctctttggaa g 31

<210> 43
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
catacttctc tttggcagac gaatctgc 28

<210> 44
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
ctccagacgt cccaaaggac tgtagagtta c 31

<210> 45
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
ctccagacgt ccagacggc tgtagagtta c 31

<210> 46
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gataccaac ttcttctgcg tctaaggctt actctg 36

<210> 47
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 47
cttctaagtc taagaagtac tctgctttg 29

<210> 48
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 48
gcttactctg ctttgattga acggattcaa aagaacgcta c 41

<210> 49
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 49
ccattcggtg aacagcaa at ggttaactc 29

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 50
gatacaaggc tctcgcgaga aacattgttc 30

<210> 51
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 51
gattgttcca ttcgtgcgcg cttctggttc 30

<210> 52
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 52
ctccagttat taacgtgatc attccagaag g 31

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
ggctgaccca ggggcccaac cacaccaagc 30

<210> 54
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
cactttggac catggtcttt gtactgcttt cg 32

<210> 55
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
gctttcgaag actctaccct aggtgacgac gttg 34

<210> 56
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
ggtgacgacg ctgaagctaa cttcac 26

<210> 57
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
ctaacttcac cgcggtgttc gctccag 27

<210> 58
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gctttgttcg ctccacctat tagagctaga ttgg 34

<210> 59
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 59
gccaggtgtt aacttgactg acgaag 26

<210> 60
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 60
gacgaagacg tcgttaactt gatggac 27

<210> 61
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 61
gtccattcga cactgtcgct agaacttc 28

<210> 62
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<220>
<223> Description of Artificial Sequence: primer

<400> 62
ctgacgctac tcagctgtct ccattc 26

<210> 63
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<220>
<223> Description of Artificial Sequence: primer

<400> 63
gtctccattc tgtgatttgc tcaactcac 28

<210> 64
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<220>
<223> Description of Artificial Sequence: primer

<400> 64
gctttgttca ccgcggacga atggag 26

<210> 65
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<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 65
cacgacgaat ggatccaata cgactac 27

<210> 66
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 66
gacgaatgga gagcgtacga ctacttg 27

<210> 67
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 67
ggtggttggtt tcgttaacga attgattgc 29

<210> 68
<211> 28
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 68
gctagattga ctcactctcc agttcaag 28

<210> 69
<211> 32
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 69
ctcacgacaa cactatgata tctattttct tc 32

<210> 70
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 70
cgacaactcc atggtttcta ttttcttcgc 30

<210> 71
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 71
gtacaacggt accaagccat tgtctac

27

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 72
ctgacgggta cgctgcttct tggac

25

<210> 73
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 73
ctgttccatt cgctgctaga gcttac

26

<210> 74
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 74
gatgcaatgt gaagctgaaa aggaacc

27

<210> 75
<211> 26
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 75
cacggttggtg gtgtcgacaa gttggg 26

<210> 76
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 76
gatctggtgg caattgggag gaatgtttcg 30

<210> 77
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 77
cacgtactcg ccatactttt cgctcgag 28

<210> 78
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 78
ccatactttt cgctcgcgga cgagctgtcc gtg 33

<210> 79
<211> 31
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 79
gtataagaag cttattacgg cgatccaggc c 31

<210> 80
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
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<400> 80
cttcaagggc aagtacgcct ttttgaagac g 31

<210> 81
<211> 29
<212> DNA
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<220>
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<400> 81
catccgagct cgcctcgaga agcatcttc 29

<210> 82
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 82
ctaattggatg tgtccgtttg atacggtag 29

<210> 83
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 83
gtggaagaag tacgactacc ttcagtc 27

<210> 84
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 84

gcccggttga cgcattcgcc agtgcagg

28

<210> 85

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 85

cacacgacaa caccatgggt tccatcttc

29

<210> 86

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 86

gtggtgcctt tcgccgcgcg agcctacttc

30

<210> 87

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 87

tatatcatga gcgtgttcgt cgtgctactg ttc

33

<210> 88

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 88

acccgactta caaagcgaat tctatagata tat

33

<210> 89
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 89
 acccttctta caaagcgaat tctatagata tat 33

<210> 90
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Consensus-phytase-3-thermo-11-Q50T

<220>
 <221> CDS
 <222> (1)..(1401)

<220>
 <221> sig_peptide
 <222> (1)..(69)

<220>
 <221> mat_peptide
 <222> (70)..(1401)

<400> 90
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 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -20 -15 -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -5 -1 1 5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20 25

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct 192
 Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40

cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct 240
 Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55

aga cac ggt gct aga tac cca act tct tct aag tct aag gct tac tct	288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser	
60 65 70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag	336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75 80 85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100 105	
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
110 115 120	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
125 130 135	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
140 145 150	
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn	
170 175 180 185	
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt	672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly	
190 195 200	
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg	
205 210 215	
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac	768
Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp	
220 225 230	
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act	816
Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac	864
Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp	
250 255 260 265	

83

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gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt 912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
                270                275                280

tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct 960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
                285                290                295

aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act 1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
                300                305                310

tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac 1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
                315                320                325

gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att 1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
                330                335                340                345

ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act 1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
                350                355                360

tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act 1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
                365                370                375

gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct 1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
                380                385                390

gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca 1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
                395                400                405

ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac 1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
                410                415                420                425

ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gct gaa 1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
                430                435                440

tgt ttc gct taa
Cys Phe Ala
2104

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<210> 91

<211> 467

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence:

Consensus-phytase-3-thermo-11-Q50T

<400> 91

Met	Gly	Val	Phe	Val	Val	Leu	Leu	Ser	Ile	Ala	Thr	Leu	Phe	Gly	Ser	-20	-15	-10
Thr	Ser	Gly	Thr	Ala	Leu	Gly	Pro	Arg	Gly	Asn	Ser	His	Ser	Cys	Asp	-5	-1	1
Thr	Val	Asp	Gly	Gly	Tyr	Gln	Cys	Phe	Pro	Glu	Ile	Ser	His	Leu	Trp	10	15	20
Gly	Thr	Tyr	Ser	Pro	Tyr	Phe	Ser	Leu	Ala	Asp	Glu	Ser	Ala	Ile	Ser	30	35	40
Pro	Asp	Val	Pro	Lys	Asp	Cys	Arg	Val	Thr	Phe	Val	Gln	Val	Leu	Ser	45	50	55
Arg	His	Gly	Ala	Arg	Tyr	Pro	Thr	Ser	Ser	Lys	Ser	Lys	Ala	Tyr	Ser	60	65	70
Ala	Leu	Ile	Glu	Ala	Ile	Gln	Lys	Asn	Ala	Thr	Ala	Phe	Lys	Gly	Lys	75	80	85
Tyr	Ala	Phe	Leu	Lys	Thr	Tyr	Asn	Tyr	Thr	Leu	Gly	Ala	Asp	Asp	Leu	90	95	100
Thr	Pro	Phe	Gly	Glu	Asn	Gln	Met	Val	Asn	Ser	Gly	Ile	Lys	Phe	Tyr	110	115	120
Arg	Arg	Tyr	Lys	Ala	Leu	Ala	Arg	Lys	Ile	Val	Pro	Phe	Ile	Arg	Ala	125	130	135
Ser	Gly	Ser	Asp	Arg	Val	Ile	Ala	Ser	Ala	Glu	Lys	Phe	Ile	Glu	Gly	140	145	150
Phe	Gln	Ser	Ala	Lys	Leu	Ala	Asp	Pro	Gly	Ser	Gln	Pro	His	Gln	Ala	155	160	165
Ser	Pro	Val	Ile	Asn	Val	Ile	Ile	Pro	Glu	Gly	Ser	Gly	Tyr	Asn	Asn	170	175	180
Thr	Leu	Asp	His	Gly	Leu	Cys	Thr	Ala	Phe	Glu	Asp	Ser	Thr	Leu	Gly	190	195	200
Asp	Asp	Val	Glu	Ala	Asn	Phe	Thr	Ala	Leu	Phe	Ala	Pro	Ala	Ile	Arg	205	210	215
Ala	Arg	Leu	Glu	Ala	Asp	Leu	Pro	Gly	Val	Thr	Leu	Thr	Asp	Glu	Asp	220	225	230
Val	Val	Tyr	Leu	Met	Asp	Met	Cys	Pro	Phe	Asp	Thr	Val	Ala	Arg	Thr	235	240	245

85

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260 265
 Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 270 275 280
 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 285 290 295
 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 300 305 310
 Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325
 Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
 330 335 340 345
 Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 350 355 360
 Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 365 370 375
 Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 380 385 390
 Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405
 Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420 425
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 430 435 440
 Cys Phe Ala

<210> 92

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence: Consensus
 phytase-3-thermo-11-Q50T-K91A

<220>

<221> sig_peptide

<222> (1)..(69)

<220>

<221> CDS

<222> (1)..(1401)

<220>

<221> mat_peptide

<222> (70)..(1401)

<400> 92

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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser	
-20 -15 -10	
aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac	96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp	
-5 -1 1 5	
act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg	144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp	
10 15 20 25	
ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct	192
Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser	
30 35 40	
cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct	240
Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser	
45 50 55	
aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct	288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser	
60 65 70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag	336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75 80 85	
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100 105	
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
110 115 120	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
125 130 135	
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
140 145 150	

87

ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn	
170 175 180 185	
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt	672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly	
190 195 200	
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg	
205 210 215	
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac	768
Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp	
220 225 230	
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act	816
Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac	864
Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp	
250 255 260 265	
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt	912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	
270 275 280	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct	960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala	
285 290 295	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act	1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr	
300 305 310	
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac	1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn	
315 320 325	
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att	1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile	
330 335 340 345	
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act	1152
Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr	
350 355 360	

88

tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act 1200
Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct 1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
380 385 390

gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca 1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac 1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

ttc	ggt	gaa	ggt	ttg	tct	ttc	gct	aga	tct	ggt	ggt	aac	tgg	gct	gaa	1392
Phe	Val	Glu	Gly	Leu	Ser	Phe	Ala	Arg	Ser	Gly	Gly	Asn	Trp	Ala	Glu	
			430						435					440		

tgt ttc gct taa
Cys Phe Ala

1404

<210> 93

<211> 467

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Consensus
phytase-3-thermo-11-Q50T-K91A

<400> 93

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro	Asp	Val	Pro	Lys	Asp	Cys	Arg	Val	Thr	Phe	Val	Gln	Val	Leu	Ser
			45					50					55		

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

89

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100 105
 Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 110 115 120
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 125 130 135
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 140 145 150
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
 170 175 180 185
 Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
 190 195 200
 Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 205 210 215
 Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
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 Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
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 Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
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 Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
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Gly	Thr	Tyr	Ser	Pro	Phe	Phe	Ser	Leu	Ala	Asp	Glu	Ser	Ala	Ile	Ser		
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75 80 85	
tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg	384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90 95 100 105	
act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac	432
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aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
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125 130 135	
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140 145 150	
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Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
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92

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gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att	1104
Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile	
330 335 340 345	
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365 370 375	
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct	1248
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380 385 390	
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca	1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro	
395 400 405	
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac	1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp	
410 415 420 425	
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gaa gaa	1392
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<400> 95

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Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
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Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
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Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
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Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
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Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
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Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
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    170                      175                      180                      185

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    205                      210                      215

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94

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Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Val	Gly	Phe	Val
			285					290					295		
Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	Pro	Val	Gln	Asp	His	Thr
		300					305					310			
Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	Ala	Thr	Phe	Pro	Leu	Asn
	315					320					325				
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Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Lys	Pro	Leu	Ser	Thr	Thr
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Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	Tyr	Ser	Ala	Ser	Trp	Thr
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Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln	Cys	Glu	Ala
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Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp	Arg	Val	Val	Pro
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Leu	His	Gly	Cys	Ala	Val	Asp	Lys	Leu	Gly	Arg	Cys	Lys	Arg	Asp	Asp
410					415					420					425
Phe	Val	Glu	Gly	Leu	Ser	Phe	Ala	Arg	Ser	Gly	Gly	Asn	Trp	Glu	Glu
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Cys Phe Ala

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Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
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tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg	384
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act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac	432
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125 130 135	

96

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Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala	
155 160 165	
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Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn	
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Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr	
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      365                      370                      375

gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct 1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
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gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca 1296
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410                      415                      420                      425

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Cys Phe Ala

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<212> PRT

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10                      15                      20                      25

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
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Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
      45                      50                      55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
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98

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 190 195 200
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 Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
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 Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
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99

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
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Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
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Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
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430 435 440

Cys Phe Ala

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 00/00025

A. CLASSIFICATION OF SUBJECT MATTER

IPC7: C12N 9/16

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC7: C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SE,DK,FI,NO classes as above

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 9949022 A1 (NOVO NORDISK A/S), 30 Sept 1999 (30.09.99), see abstract, sequences, 100% homology --	1-14
P,X	WO 9948380 A1 (NOVO NORDISK A/S), 30 Sept 1999 (30.09.99), see abstract, sequences, 100% homology --	1-14
P,X	EP 0897985 A2 (F. HOFFMANN-LA ROCHE AG), 24 February 1999 (24.02.99), see figure 3, page 13, lines 10-11, sequences --	1-14
A	EP 0422697 A1 (AMGEN INC.), 17 April 1991 (17.04.91) --	1-14



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

4 May 2000

Date of mailing of the international search report

17-05-2000

Name and mailing address of the ISA:

Swedish Patent Office
Box 5055, S-102 42 STOCKHOLM
Facsimile No. +46 8 666 02 86

Authorized officer

Yvonne Sjösteen/EÖ
Telephone No. +46 8 782 25 00

INTERNATIONAL SEARCH REPORT

International application No.

PCT/DK 00/00025

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 9735016 A1 (NOVO NORDISK BIOTECH, INC.), 25 Sept 1997 (25.09.97), see page 10, line 22 - page 11, line 18 --	1-14
A	EP 0420358 A1 (GIST-BROCADES N.V.), 3 April 1991 (03.04.91), see page 10, line 6 - line 14 and claims 66% homology -- -----	1-14

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 00/00025

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: **Part of claims 1 and 5**
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).:

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 00/00025

In claim 1 SEQ ID NO:26 is said to be 467 amino acids long whereas in the Sequence listing it is only composed of 441 amino acids.
In claim 5 SEQ ID NO:29 is said to be 1407 nucleotides long whereas in the Sequence listing it is only composed of 1404 nucleotides.

The search has been performed on the sequences as they are described in the Sequence listing.

INTERNATIONAL SEARCH REPORT

Information on patent family members

02/12/99

International application No.

PCT/DK 00/00025

Patent document cited in search report			Publication date	Patent family member(s)	Publication date
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